GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 10, 2003, 22:54:36 ; Search time 8032 Seconds
(without alignments)
8551.701 Million cell updates/sec

Title: US-10-017-084A-522
Perfect score: 1679
Sequence: 1 gttgtgtccttcagcaaaac.....ataaaaagagcaaaaaaaaa 1679

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1679	100.0	1679	6	AX358872	AX358872 Sequence
2	1679	100.0	1679	6	AX362365	AX362365 Sequence
3	1679	100.0	1679	6	AX403748	AX403748 Sequence
4	1679	100.0	1679	6	AX454470	AX454470 Sequence
5	1679	100.0	1679	6	AX464242	AX464242 Sequence
6	1679	100.0	1679	6	AX490948	AX490948 Sequence
7	1432.8	85.3	1839	6	AX665342	AX665342 Sequence
8	1432.8	85.3	1839	9	AF126426	AF126426 Homo sapi
9	996.8	59.4	2040	10	RNU16845	U16845 Rattus norv
10	976.4	58.2	1615	10	BC023307	BC023307 Mus muscu
11	910.6	54.2	1410	10	AF282980	AF282980 Mus muscu
12	910.4	54.2	1068	6	AX665344	AX665344 Sequence
13	874.4	52.1	1104	6	AX665346	AX665346 Sequence
14	856	51.0	1325	9	BC050716	BC050716 Homo sapi
15	851.8	50.7	1140	6	AX665348	AX665348 Sequence
16	643.8	38.3	1058	5	AF292935	AF292935 Gallus ga
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18	638.2	38.0	1035	5	AB011810	AB011810 Gallus ga
19	623.6	37.1	1638	12	AF271233	AF271233 Synthetic
c 20	609.8	36.3	202505	2	AP000912	AP000912 Homo sapi
c 21	608.2	36.2	184716	2	AC018368	AC018368 Homo sapi
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23	604.8	36.0	1013	5	AF292936	AF292936 Gallus ga
24	595.4	35.5	187203	2	AP000832	AP000832 Homo sapi
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26	551.8	32.9	1556	5	AF292934	AF292934 Gallus ga
27	545.4	32.5	2593	4	BTOBCAM	X12672 Bovine mRNA
28	540.8	32.2	3069	10	RATCALMA	M88709 Rattus norv
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31	523	31.1	2179	10	RATCALMB	M88710 Rattus norv
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34	465.2	27.7	2935	12	AF271618	AF271618 Synthetic
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36	441.2	26.3	452	6	AX079423	AX079423 Sequence
37	435.4	25.9	756	12	AF271232	AF271232 Synthetic
38	362	21.6	1107	5	GGLAMPG9	Z94718 G.gallus mR
39	359.2	21.4	1158	5	GGLAMPG19	Z94720 G.gallus mR
40	357.6	21.3	2050	5	GGE19SPRO	Y08171 Gallus gall
41	348.4	20.8	1194	5	GGLAMPG11	Z94719 G.gallus mR
42	347.4	20.7	1640	9	BC033803	BC033803 Homo sapi
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44	343	20.4	1238	6	AR220258	AR220258 Sequence
45	343	20.4	1238	10	RNU31554	U31554 Rattus norv

ALIGNMENTS

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AX358872
LOCUS AX358872 1679 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 125 from Patent WO0193983.
ACCESSION AX358872
VERSION AX358872.1 GI:18675337
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V.I., Stephan,J.P.,
Watanabe,C.K. and Wood,W.I.

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  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
  JOURNAL   Patent: WO 0193983-A 125 13-DEC-2001;
            Genentech Inc. (US)
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
BASE COUNT     498 a    432 c    419 g    330 t
ORIGIN

  Query Match           100.0%;  Score 1679;  DB 6;  Length 1679;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1679;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60

Qy         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120
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RESULT 2
AX362365
LOCUS       AX362365               1679 bp    DNA     linear   PAT 15-FEB-2002
DEFINITION  Sequence 125 from Patent WO0208288.
ACCESSION   AX362365
VERSION     AX362365.1  GI:18694640
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,
            Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
            Watanabe,C.K. and Wood,W.I.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
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  JOURNAL   Patent: WO 0208288-A 125 31-JAN-2002;
            Genentech, Inc. (US)
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BASE COUNT      498 a    432 c    419 g    330 t
ORIGIN

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  Matches 1679;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy       1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620
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Qy       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
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Db       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679

RESULT 3
AX403748
LOCUS       AX403748               1679 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 103 from Patent WO0077037.
ACCESSION   AX403748
VERSION     AX403748.1  GI:21437184
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ashkenazi,A., Baker,K., Botstein,D., Desnoyers,L., Eaton,D.L.,
            Ferrara,N., Fong,S., Gao,W.Q., Gerber,H., Gerritsen,M.E.,
            Goddard,A., Godowski,P., Gurney,A., Kljavin,I.J., Mather,J.,
            Napier,M., Pan,J., Paoni,N., Roy,M., Tumas,D., Watanabe,C.,
            Williams,P.M., Wood,W.I. and Zhang,Z.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
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  JOURNAL   Patent: WO 0077037-A 103 21-DEC-2000;
            Genentech Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1679
                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
BASE COUNT      498 a    432 c    419 g    330 t
ORIGIN

  Query Match           100.0%;  Score 1679;  DB 6;  Length 1679;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1679;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60

Qy         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120
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Qy        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240
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Qy        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420
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Db        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720

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Db        841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900

Qy        901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960
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Db        901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960

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Db       1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080

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Db       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320

Qy       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380
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Db       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380

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Qy       1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620
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Qy       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
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RESULT 4
AX454470
LOCUS       AX454470                1679 bp    DNA     linear   PAT 06-JUL-2002
DEFINITION  Sequence 55 from Patent WO0208284.
ACCESSION   AX454470
VERSION     AX454470.1  GI:21713859
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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REFERENCE   1
  AUTHORS   Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
            Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
            Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
            and Ye,W.
  TITLE     Compositions and methods for the diagnosis and treatment of
            disorders involving angiogenesis
  JOURNAL   Patent: WO 0208284-A 55 31-JAN-2002;
```

Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone (US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard, Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ; Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US) ; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ; Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William I. (US)

FEATURES Location/Qualifiers
source 1. .1679
/organism="Homo sapiens"
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BASE COUNT 498 a 432 c 419 g 330 t
ORIGIN

Query Match 100.0%; Score 1679; DB 6; Length 1679;
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Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
AX464242
LOCUS AX464242 1679 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 375 from Patent WO0140466.
ACCESSION AX464242
VERSION AX464242.1 GI:21899137
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Baker,K.P., Beresini,M., Deforge,L., Desnoyers,L., Filvaroff,E., Gao,W.Q., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L.,

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            Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K.,
            Wood,W.L. and Zhang,Z.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            same
  JOURNAL   Patent: WO 0140466-A 375 07-JUN-2001;
            Genentech Inc. (US)
FEATURES             Location/Qualifiers
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BASE COUNT      498 a    432 c    419 g    330 t
ORIGIN

  Query Match          100.0%;  Score 1679;  DB 6;  Length 1679;
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Qy        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300
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Qy        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
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Qy        481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540
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Db        481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540

Qy        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
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Db        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600

Qy        601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660
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Db        601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660

Qy        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
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Db        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720

Qy        721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAA 780
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Qy        841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900
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Db        841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900

Qy        901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960
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Db        901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960

Qy        961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020
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Qy       1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200
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Qy       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
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Qy       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320
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Db       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320

Qy       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380
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Db       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380

Qy       1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440
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Qy       1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500
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Qy       1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560
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Qy       1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620
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Db       1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620

Qy       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
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RESULT 6
AX490948
LOCUS       AX490948               1679 bp    DNA     linear   PAT 16-AUG-2002
DEFINITION  Sequence 55 from Patent WO0200690.
ACCESSION   AX490948
VERSION     AX490948.1  GI:22323811
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
            Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
            Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
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            and Ye,W.
  TITLE     Compositions and methods for the diagnosis and treatment of
            disorders involving angiogenesis
  JOURNAL   Patent: WO 0200690-A 55 03-JAN-2002;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1679
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT      498 a    432 c    419 g    330 t
ORIGIN

  Query Match           100.0%;  Score 1679;  DB 6;  Length 1679;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1679;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60

Qy         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120
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Db         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120

Qy        121 AAGAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180
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Db        121 AAGAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180

Qy        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240
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Db        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240

Qy        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300
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Qy        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
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Qy        421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
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Qy        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
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Db        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600

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Qy        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
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Qy        901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960
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Qy       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
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Qy       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320
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Qy       1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560
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Db       1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560

Qy       1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620
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Db       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679


RESULT 7
AX665342
LOCUS       AX665342               1839 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 100 from Patent WO03002765.
ACCESSION   AX665342
VERSION     AX665342.1  GI:29290464
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Sellar,G.C. and Gabra,H.
  TITLE     Cancer
  JOURNAL   Patent: WO 03002765-A 100 09-JAN-2003;
            Cancer Research Technology Limited (GB)
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FEATURES             Location/Qualifiers
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BASE COUNT      464 a    506 c    503 g    366 t
ORIGIN

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  Best Local Similarity   98.5%;  Pred. No. 0;
  Matches 1464;  Conservative    0;  Mismatches    2;  Indels   20;  Gaps    1;

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Db        345 AGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGT 404

Qy        274 CCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGC 333
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Db        405 CCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGC 464

Qy        334 CTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCG 393
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Db        465 CTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCG 524

Qy        394 CGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGT 453
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Db        525 CGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGT 584

Qy        454 GTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAG 513
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Db        585 GTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAG 644

Qy        514 GGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCAT 573
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Db        645 GGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCAT 704

Qy        574 TAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGT 633
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Db        705 TAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGT 764

Qy        634 TACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGA 693
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Qy        694 AATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGT 753
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Qy        754 GGCCGCGCCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGA 813
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Qy        814 AGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGC 873
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Qy        994 ACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAG 1053
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Qy       1054 CATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGC 1113
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Qy       1114 AGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGATGTGA 1173
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Db       1245 AGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGATGTGA 1304

Qy       1174 GTGCCACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATG 1233
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Db       1305 GTGCCACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATG 1364

Qy       1234 GCAACACCGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCA 1293
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Qy       1294 TGGGACAGAAATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAAAGAGTTTTAAAA 1353
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Qy       1354 AAGAAATTGAAAATTGCCTTGCAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACG 1413
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Db       1485 AAGAAATTGAAAATTGCCTTGCAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACG 1544

Qy       1414 GGAAGAACACAGCACACCCGGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGG 1473
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Db       1545 GGAAGAACACAGCACACCCGGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGG 1604

Qy       1474 TGCCAGTGTGGGCAAGGGCTCAGCCTCTCTGCCCACAGAGTGCCCCCACGTGGAACATTC 1533
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Qy       1534 TGGAGCTGGCCATCCCAAATTCAATCAGTCCATAGAGACGAACAGAATGAGAC------- 1586
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Db       1665 TGGAGCTGGCCATCCCAAATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGG 1724

Qy       1587 -------------CTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTGGTAGACTGTGCCA 1633
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Db       1725 CCCAAGCGTGGCGCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTGGTAGACTGTGCCA 1784

Qy       1634 CCACGGCGTGTGTTGTGAAACGTGAAATAAAAAAGAGCAAAAAAAAA 1679
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Db       1785 CCACGGCGTGTGTTGTGAAACGTGAAATAAAAAAGAGCAAAAAAAAA 1830


RESULT 8
AF126426
LOCUS       AF126426               1839 bp    mRNA    linear   PRI 10-JUN-2002
DEFINITION  Homo sapiens neurotrimin (HNT) mRNA, complete cds.
ACCESSION   AF126426
VERSION     AF126426.1  GI:7158997
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1839)
  AUTHORS   Li,G., Jin,J., Tan,X., Hu,S., Yuan,J. and Qiang,B.
  TITLE     Cloning and identification of human neurotrimin full length cDNA
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1839)
  AUTHORS   Li,G., Jin,J., Tan,X., Hu,S., Yuan,J. and Qiang,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-FEB-1999) Biochemistry, Institute of Basic Medical
            Sciences, 5 Dong Dan San Tiao, Beijing 100005, PR China
FEATURES             Location/Qualifiers
     source          1. .1839
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     CDS             265. .1299
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                     /product="neurotrimin"
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                 GRPEPTVTWRHISPKAVGFVSEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVT
                 VNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPF
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                 LLVLHLLLKF"
BASE COUNT      464 a    506 c    503 g    366 t
ORIGIN

  Query Match          85.3%;  Score 1432.8;  DB 9;  Length 1839;
  Best Local Similarity   98.5%;  Pred. No. 0;
  Matches 1464;  Conservative    0;  Mismatches    2;  Indels   20;  Gaps    1;

Qy        214 AGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGT 273
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Db        345 AGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGT 404

Qy        274 CCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGC 333
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Db        405 CCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGC 464

Qy        334 CTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCG 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 CTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCG 524

Qy        394 CGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGT 453
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Db        525 CGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGT 584

Qy        454 GTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAG 513
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Qy        514 GGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCAT 573
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Db        645 GGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCAT 704

Qy        574 TAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGT 633
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Db        705 TAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGT 764

Qy        634 TACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGA 693
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Db        765 TACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGA 824

Qy        694 AATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGT 753
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Db        825 AATTCAGGGCATCACCCGGGAACAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGT 884

Qy        754 GGCCGCGCCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGA 813
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Qy        814 AGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGC 873
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Db        945 AGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGC 1004

Qy        874 AGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAA 933
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Db       1005 AGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAA 1064

Qy        934 AGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGA 993
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Db       1065 AGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGA 1124

Qy        994 ACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAG 1053
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Db       1125 ACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAG 1184

Qy       1054 CATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGC 1113
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Db       1185 CATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGC 1244

Qy       1114 AGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGATGTGA 1173
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Db       1245 AGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGATGTGA 1304

Qy       1174 GTGCCACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCACCACCAACACAACAGCAATG 1233
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Db       1305 GTGCCACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCACCAACACAACAGCAATG 1364

Qy       1234 GCAACACCGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCA 1293
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Db       1365 GCAACACCGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCA 1424

Qy       1294 TGGGACAGAAATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAAAGAGTTTTAAAA 1353
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Db       1425 TGGGACAGAAATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAAAGAGTTTTAAAA 1484

Qy       1354 AAGAAATTGAAAATTGCCTTGCAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACG 1413
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Db       1485 AAGAAATTGAAAATTGCCTTGCAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACG 1544

Qy       1414 GGAAGAACACAGCACACCCGGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGG 1473
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Qy       1534 TGGAGCTGGCCATCCCAAATTCAATCAGTCCATAGAGACGAACAGAATGAGAC------- 1586
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Db       1665 TGGAGCTGGCCATCCCAAATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGG 1724

Qy       1587 ------------CTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTGGTAGACTGTGCCA 1633
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Db       1725 CCCAAGCGTGGCGCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTGGTAGACTGTGCCA 1784

Qy       1634 CCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
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Db       1785 CCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1830


RESULT 9
RNU16845
LOCUS       RNU16845               2040 bp    mRNA    linear   ROD 26-MAY-1995
DEFINITION  Rattus norvegicus neurotrimin mRNA, complete cds.
ACCESSION   U16845
VERSION     U16845.1  GI:755184
KEYWORDS    .
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 2040)
  AUTHORS   Struyk,A.F., Canoll,P.D., Wolfgang,M.J., Rosen,C.L., D'Eustachio,P.
            and Salzer,J.L.
  TITLE     Cloning of neurotrimin defines a new subfamily of differentially
            expressed neural cell adhesion molecules
  JOURNAL   J. Neurosci. 15 (3 Pt 2), 2141-2156 (1995)
  MEDLINE   95198094
  PUBMED    7891157
REFERENCE   2  (bases 1 to 2040)
  AUTHORS   Salzer,J.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-NOV-1994) James L. Salzer, Cell Biology, NYU Medical
            Center, 550 First Avenue, New York, NY 10016, USA
FEATURES             Location/Qualifiers
     source          1..2040
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                     GRPEPTVTWRHISPKAVGFVSEDEYLEIQGITREQSGEYECSASNDVAAPVVRRVNVT
                     VNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWFKDDKRLVEGKKGVKVENRPF
                     LSRLTFFNVSEHDYGNYTCVASNKLGHTNASIMLFGPGAVSEVNNGTSRRAGCIWLLP
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BASE COUNT      504 a    544 c    551 g    441 t
ORIGIN

  Query Match           59.4%;  Score 996.8;  DB 10;  Length 2040;
  Best Local Similarity   84.3%;  Pred. No. 1.2e-253;
  Matches 1249;  Conservative    0;  Mismatches  202;  Indels   31;  Gaps   10;

Qy        214 AGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGT 273
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Db        564 AGGAGTGCCGGTGCGTAGCGGAGATGCCACCTTTCCCAAAGCTATGGACAACGTGACGGT 623

Qy        274 CCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGC 333
              | |||||||||||||||||||||||||||||||| |||||||||| ||||||||||||
Db        624 CAGGCAGGGGGAGAGCGCCACCCTCAGGTGCACAATTGACAACCGAGTCACCCGGGTGGC 683

Qy        334 CTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCG 393
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Db        684 CTGGCTAAACCGCAGTACCATCCTCTATGCTGGAAATGACAAGTGGTGCCTAGATCCTCG 743

Qy        394 CGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGT 453
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Db        744 TGTGGTTCTCCTGAGTAACACCCAGACCCAGTACAGCATTGAGATCCAGAATGTGGATGT 803

Qy        454 GTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAG 513
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Db        804 GTATGATGAGGGCCCTTATACCTGCTCGGTGCAGACAGACAACCACCCTAAGACCTCCAG 863

Qy        514 GGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCAT 573
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Db        864 GGTCCACCTCATTGTACAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCAT 923

Qy        574 TAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGT 633
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Qy        634 TACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGA 693
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Db        984 AACCTGGAGACATATTTCTCCCAAAGCTGTCGGCTTTGTGAGTGAGGATGAGTACCTGGA 1043

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Db       1044 GATCCAGGGCATCACTCGGGAGCAGTCAGGCGAGTATGAGTGCAGCGCCTCCAACGACGT 1103

Qy        754 GGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGA 813
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Db       1104 GGCAGCACCAGTCGTACGAAGAGTGAACGTCACCGTGAACTATCCACCATACATCTCAGA 1163

Qy        814 AGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGC 873
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Db       1164 AGCTAAGGGTACAGGTGTCCCCGTGGGGCAGAAGGGGACTCTGCAGTGTGAAGCCTCGGC 1223

Qy        874 AGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAA 933
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Db       1224 AGTCCCTTCAGCAGAATTTCAGTGGTTCAAGGATGACAAAAGACTGGTTGAAGGGAAGAA 1283

Qy        934 AGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGA 993
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Db       1284 GGGAGTCAAAGTGGAAAACAGACCTTTCCTTTCAAGACTCACCTTTTTCAACGTCTCTGA 1343

Qy        994 ACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAG 1053
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Db       1344 ACACGACTATGGGAACTACACATGTGTGGCATCCAACAAGTTGGGCCACACCAATGCCAG 1403

Qy       1054 CATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGC 1113
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Qy       1114 AGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGATGTGA 1173
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Db       1464 AGGCTGCATTTGGCTCCTCCCTCTTCTGGTCTTACACCTGCTCCTCAAATTTTGATGTGA 1523

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Qy       1234 GCAACACCGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCA 1293
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Db       1581 -------CAACATGAAGCAACAAGTCAGAATCAAATGAAATTCCGAGAATCACAGCC-AA 1632

Qy       1294 TGGGACAGAAATTTGAGGGAGGGGAACAAAGAATACTTTGGGG----------GGAAAAGA 1344
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Db       1633 TGAGACAGAAATTCGAGGGAGGGGAACAAAGCATACTGTGGTAAAGGGGAAAAAAAAAGT 1692

Qy       1345 GTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATATTTAGGTACAATGGAGT----TTT 1400
                |  ||||  || ||||||||||||||||||| |||| ||||| |  ||||    |||
Db       1693 CTAAAAAAAGGAAATTTGAAAATTGCCTTGCAGACATTTCGGTACCACTGAGTTTTCTTT 1752

Qy       1401 CTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGACCCA-CTGCAAGCTGCATCG 1459
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Qy       1460 TGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTCTCTGCCCAC-AGAGTGCCC 1518
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Db       1810 TGTGACCTCTCTGTTGCCAGGGTGGGCAAGGGCTCAGCCACTCTGCCCACTAAAGTGCCC 1869

Qy       1519 CCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCAGTCCATAGAGAC--GAAC 1576
              |  | ||||||||||||||  ||||||||||||||  ||| |||||||||  ||  | ||
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Db       1930 AGAGTGAGAAACAGGGGCCCAGAAGTGCCACGGAGGGCCCTTTGGTGGGCTGCGCGATGG 1989

Qy       1637 CGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAA 1678
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Db       1990 TGGCGTGTGTCATGAAGTGTGAAATCCGAAGTAGAAAAAAAA 2031


RESULT 10
BC023307
LOCUS       BC023307               1615 bp    mRNA    linear   ROD 10-JUN-2003
DEFINITION  Mus musculus neurotrimin, mRNA (cDNA clone MGC:30504
            IMAGE:4480983), complete cds.
ACCESSION   BC023307
VERSION     BC023307.1  GI:23958300
KEYWORDS    MGC.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1615)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
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            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
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            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1615)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-FEB-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: The Cepko Laboratory
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: amg@bcm.tmc.edu
            Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
            Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
            A.N., Gibbs, R.A.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 41 Row: h Column: 10
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 26986610.
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                    /tissue_type="Eye, retina, mouse strain C57Bl\6"
                    /clone_lib="NIH_MGC_94"
                    /lab_host="DH10B"
                    /note="Vector: pCMV-SPORT6"
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                    /db_xref="LocusID:235106"
                    /db_xref="MGI:2446259"
     CDS            44. .1078
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                    /protein_id="AAH23307.1"
                    /db_xref="GI:23958301"
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                    GRPEPTVTWRHISPKAVGFVSEDEYLEIQGITREQSGEYECSASNDVAAPVVRRVKVT
                    VNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWFKDDKRLVEGKKGVKVENRPF
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BASE COUNT      442 a    403 c    428 g    342 t
ORIGIN

  Query Match           58.2%;  Score 976.4;  DB 10;  Length 1615;
  Best Local Similarity  83.4%;  Pred. No. 2.9e-248;
  Matches 1234;  Conservative    0;  Mismatches  221;  Indels   25;  Gaps   10;
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Qy      214 AGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGT 273
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Qy      334 CTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCG 393
Db      244 CTGGCTAAACCGCAGTACCATCCTCTATGCTGGAAATGACAAGTGGTGCCTAGATCCTCG 303

Qy      394 CGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGT 453
Db      304 TGTGGTCCTCCTGAGTAACACCCAGACCCAGTACAGCATTGAGATCCAGAATGTGGATGT 363

Qy      454 GTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAG 513
Db      364 GTACGATGAGGGCCCTTATACCTGCTCGGTACAGACAGACAACCACCCTAAGACCTCCAG 423

Qy      514 GGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCAT 573
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Qy      574 TAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGT 633
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Qy      874 AGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAA 933
Db      784 AGTCCCTTCAGCAGAATTTCAATGGTTCAAGGATGACAAAAGACTGGTCGAAGGAAAGAA 843

Qy      934 AGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGA 993
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Db     1024 AGGCTGCATTTGGCTCCTCCCTCTTCTGGTCTTACACCTGCTCCTCAAATTTTGATGTGA 1083

Qy     1174 GTGCCACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATG 1233
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Qy     1234 GCAACACCGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCA 1293
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Qy     1294 TGGGACAGAAATTTGAGGGAGGGGAACAAAGAATACTTTG-----GGGGGAAAAGAGTTT 1348
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Db       1193 TGAGACAGAAATTCGAGGGAGGGGGACAAAGCATACTGTGGTAAAGGGGAAAAAAAGGTT 1252

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Qy       1464 ACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTCTCTGCCCAC-AGAGTGCCCCCAC 1522

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Qy       1640 CGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679

Db       1553 CGTGTGTCATGAAGTGTGAAATCTGGAGGAAGAAAAAAA 1592


RESULT 11
AF282980
LOCUS       AF282980                1410 bp    mRNA    linear   ROD 01-FEB-2001
DEFINITION  Mus musculus neurotrimin mRNA, complete cds.
ACCESSION   AF282980
VERSION     AF282980.1  GI:12642539
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1410)
  AUTHORS   Kim,T.H., Choi,S.C., Kim,J., Jeon,J.W., Kim,K.D. and Lee,S.H.
  TITLE     Cloning and expression of mouse neurotrimin gene in the developing
            nervous system
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1410)
  AUTHORS   Kim,T.H., Choi,S.C., Kim,J., Jeon,J.W., Kim,K.D. and Lee,S.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-JUN-2000) Graduate School of Biotechnology, Korea
            University, 1,5-ka Anam-dong Sungbuk-ku, Seoul 136-701, Korea
FEATURES             Location/Qualifiers
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  Best Local Similarity  84.6%;  Pred. No. 9.2e-231;
  Matches 1134;  Conservative    0;  Mismatches  184;  Indels   23;  Gaps    9;

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Db        381 GGTCCACCTCATTGTACAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCAT 440

Qy        574 TAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGT 633

Db        441 TAATGAAGGGAACAACATCAGCCTCACTTGCATAGCCACAGGTAGGCCGGAGCCTACAGT 500

Qy        634 TACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGA 693

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Qy        994 ACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAG 1053

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RESULT 12
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LOCUS AX665344 1068 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 102 from Patent WO03002765.
ACCESSION AX665344
VERSION AX665344.1 GI:29290465
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Sellar,G.C. and Gabra,H.
TITLE Cancer
JOURNAL Patent: WO 03002765-A 102 09-JAN-2003;
Cancer Research Technology Limited (GB)
FEATURES Location/Qualifiers
source 1. .1068
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ORIGIN

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Best Local Similarity 96.6%; Pred. No. 9.6e-231;
Matches 954; Conservative 0; Mismatches 1; Indels 33; Gaps 1;

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Db         81 AGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGT 140

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Qy        334 CTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCG 393

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Qy        574 TAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGT 633

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Db        561 AATTCAGGGCATCACCCGGGAACAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGT 620

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Db       1041 GGTCTTGCACCTGCTTCTCAAATTTTGA 1068
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RESULT 13
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LOCUS AX665346 1104 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 104 from Patent WO03002765.
ACCESSION AX665346
VERSION AX665346.1 GI:29290466
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Sellar,G.C. and Gabra,H.
TITLE Cancer
JOURNAL Patent: WO 03002765-A 104 09-JAN-2003;
Cancer Research Technology Limited (GB)
FEATURES Location/Qualifiers
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/db_xref="taxon:9606"
BASE COUNT 280 a 298 c 294 g 232 t
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Query Match 52.1%; Score 874.4; DB 6; Length 1104;

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Qy        274 CCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGC 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 CCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGC 200

Qy        334 CTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCG 393
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Db        201 CTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCG 260

Qy        394 CGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGT 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        514 GGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCAT 573
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Db        381 GGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCAT 440

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Qy        634 TACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGA 693
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGA 560

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Db        561 AATTCAGGGCATCACCCGGGAACAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGT 620

Qy        754 GGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGA 813
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Db        621 GGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGA 680

Qy        814 AGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGC 873
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Qy        874 AGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAA 933
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Qy        934 AGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGA 993
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Db        801 AGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGA 860

Qy        994 ACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAG 1053
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Db        861 ACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAG 920

Qy       1054 CATCATGCTATTT---------------------------------------------- 1066
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Db        921 CATCATGCTATTTGAACTAAATGAGCCTACGAGCTCAACTTTGTTGCAAGAAGTGAAAAC 980

Qy       1067 ----------------------GGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTC 1104
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Db        981 TACAGCCCTGACCCCTTGGAAAGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTC 1040

Qy       1105 GAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATT 1164
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Qy       1165 TTGA 1168
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Db       1101 TTGA 1104
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RESULT 14
BC050716
LOCUS       BC050716               1325 bp    mRNA    linear   PRI 22-APR-2003
DEFINITION  Homo sapiens mRNA similar to neurotrimin (cDNA clone MGC:60329
            IMAGE:6166839), complete cds.
ACCESSION   BC050716
VERSION     BC050716.1  GI:30047134
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1325)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
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            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
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            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1325)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-APR-2003) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 110 Row: m Column: 8
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 7705412.
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                     GRPEPTVTWRHISPKAVGFVSEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVT
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BASE COUNT      398 a    295 c    375 g    257 t
ORIGIN

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  Matches  856;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        214 AGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGT 273
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Qy        274 CCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGC 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        155 CCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGC 214

Qy        334 CTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCG 393
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Qy        394 CGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGT 453
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Qy        454 GTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAG 513
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Qy        634 TACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGA 693
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Qy        694 AATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGT 753
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Qy       1054 CATCATGCTATTTGGT 1069
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RESULT 15
AX665348
LOCUS       AX665348               1140 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 106 from Patent WO03002765.
ACCESSION   AX665348
VERSION     AX665348.1  GI:29290467
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Sellar,G.C. and Gabra,H.
  TITLE     Cancer
  JOURNAL   Patent: WO 03002765-A 106 09-JAN-2003;
            Cancer Research Technology Limited (GB)
FEATURES             Location/Qualifiers
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BASE COUNT      289 a    304 c    304 g    243 t
ORIGIN

  Query Match           50.7%;  Score 851.8;  DB 6;  Length 1140;
  Best Local Similarity  99.8%;  Pred. No. 3.8e-215;
  Matches  853;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        214 AGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGT 273
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Search completed: September 11, 2003, 01:36:37
Job time : 8040 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 10, 2003, 23:11:32 ; Search time 4332 Seconds
(without alignments)
9419.948 Million cell updates/sec

Title: US-10-017-084A-522
Perfect score: 1679
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: em_esthum:*
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28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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3	733.4	43.7	1033	12	BM807426	BM807426 AGENCOURT
4	720.2	42.9	1083	12	BM809227	BM809227 AGENCOURT
5	674	40.1	865	12	BI666583	BI666583 603291469
6	664.8	39.6	856	13	BU155617	BU155617 AGENCOURT
7	645	38.4	1085	9	AL533026	AL533026 AL533026
8	643	38.3	732	12	BI551784	BI551784 603197479
9	635.2	37.8	1039	10	BE798585	BE798585 601581610
10	628.4	37.4	784	12	BI549918	BI549918 603194765
11	621.2	37.0	870	12	BI913885	BI913885 603183295
12	619.6	36.9	765	14	CD354474	CD354474 UI-M-GM0-
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c 14	602.4	35.9	604	9	AW025115	AW025115 wu71h04.x
c 15	598.8	35.7	602	13	BU741589	BU741589 UI-E-EO1-
c 16	594.8	35.4	770	9	AW117456	AW117456 xd92a06.x
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22	531.4	31.6	545	10	BE263639	BE263639 601192064
23	522	31.1	534	12	BM686717	BM686717 UI-E-CQ0-
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25	488.8	29.1	660	14	BY723873	BY723873 BY723873
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27	486.8	29.0	910	13	BX432064	BX432064 BX432064
28	485.6	28.9	953	12	BM423716	BM423716 AGENCOURT
29	479.8	28.6	671	10	BB644996	BB644996 BB644996
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32	469	27.9	522	12	BI553032	BI553032 603193672
33	465.6	27.7	479	9	AA843782	AA843782 aj18d10.s
34	457.4	27.2	524	10	BE014142	BE014142 125737 MA
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38	454.6	27.1	890	14	CD327172	CD327172 AGENCOURT
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c 42	445	26.5	456	9	AI369684	AI369684 qy71g03.x
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44	443.8	26.4	655	12	BI548049	BI548049 603196558
c 45	439	26.1	440	9	AI318423	AI318423 qo53g09.x

ALIGNMENTS

RESULT 1
AK045973
LOCUS AK045973 1808 bp mRNA linear HTC 05-DEC-2002
DEFINITION Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230328N06 product:NEUROTRIMIN PRECURSOR (GP65) homolog [Rattus norvegicus], full insert sequence.
ACCESSION AK045973
VERSION AK045973.1 GI:26337738
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159

REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
MEDLINE 21085660
PUBMED 11217851
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 1808)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
FEATURES Location/Qualifiers

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ORIGIN

Query Match 66.7%; Score 1119.4; DB 11; Length 1808;
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VERSION AK046377.1 GI:26338018
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REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
MEDLINE 21085660
PUBMED 11217851
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

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JOURNAL     Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 1808)
AUTHORS     Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
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            Muramatsu,M. and Hayashizaki,Y.
TITLE       Direct Submission
JOURNAL     Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.go.jp/
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Qy        769 ACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGG 828
Db        839 ACGAAGAGTGAAGGTCACCGTGAACTATCCACCATACATCTCAGAAGCTAAGGGCACAGG 898

Qy        829 TGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGA 888
Db        899 TGTCCCCGTGGGGCAGAAGGGGACTCTGCAGTGTGAAGCTTCCGCAGTCCCTTCAGCAGA 958

Qy        889 ATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGA 948
Db        959 ATTTCAATGGTTCAAGGATGACAAAAGACTGGTCGAAGGAAAGAAGGGAGTCAAAGTGGA 1018

Qy        949 AAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAA 1008
Db       1019 AAACAGACCTTTCCTTTCAAAACTCACCTTTTTCAACGTCTCTGAACATGACTATGGGAA 1078

Qy       1009 CTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGG 1068
Db       1079 CTACACATGTGTGGCCTCCAACAAGCTGGGTCACACCAACGCCAGCATCATGCTATTTGG 1138

Qy       1069 TCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCT 1128
Db       1139 TCCCGGTGCTGTCAGTGAGGTCAACAATGGGACATCAAGGAGGGCAGGCTGCATTTGGCT 1198

Qy       1129 GCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCAC 1188
Db       1199 CCTCCCTCTTCTGGTCTTACACCTGCTCCTCAAATTTTGATGTGAGTGCCCCTTCCCTGC 1258

Qy       1189 CCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCA 1248
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Db       1259 TGGGGAGA-GCTGCTGCCACCGCATC--TCAATACAACAGCACTG-------CAAAATGA 1308

Qy       1249 ACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTG 1308
              | ||| ||  | |  ||||||||||||   |||| |||||||| ||| |||||||||| |
Db       1309 AGCAACAAGTCAGAATCAAATGAAATTCCGAGAATCACAGCC-AATGAGACAGAAATTCG 1367

Qy       1309 AGGGAGGGGAACAAAGAATACTTTG-----GGGGGAAAAGAGTTTTAAAAAAG---AAAT 1360
              ||||||| | |||||| ||||| ||     |||| |||| || ||||| |||   || | .
Db       1368 AGGGAGGAGGACAAAGCATACTGTGGTAAAGGGGAAAAAAAGGTTTAAGAAAAGGAAATT 1427

Qy       1361 TGAAAATTGCCTTGCAGATATTTAGGTACAATGGAGTTTTCTTT-TCCCAAACGGGAAGA 1419
              || |||||||||||||||||||| |||||    ||||||||||| |         |   ||
Db       1428 TGGAAATTGCCTTGCAGATATTTCGGTACCGCTGAGTTTTCTTTCTTTTCCCAAGTGGGA 1487

Qy       1420 ACACAGCACACCCGGCTTGGACCCA-CTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCA 1478
              | |  |||||||  |||||||||||  | |||||||||  |||  |||||| || |||||
Db       1488 AGAAGGCACACCTAGCTTGGACCCACCCACAAGCTGCACTGTGTGACCTCTCTGTTGCCA 1547

Qy       1479 GTGTGGGCAAGGGCTCAGCCTCTCTGCCCAC-AGAGTGCCCCCACGTGGAACATTCTGGA 1537
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Db       1548 GGGTGGGCAAGGGCTCAGCCACTCTGCCCACTAAAGTGCCCCACCATGAAACATTCTGGA 1607

Qy       1538 GCTGGCCATCCCAAATTCAATCAGTCCATAGAGACGAACAGAATG---AGACCTTCCGGC 1594
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Db       1608 GTTGGCCATCCCAAATTTCATCGGTCCATAGACACAAGCACAGAGCAAGAAACAAGGGCC 1667

Qy       1595 CCAAGCGTGGCGCTGCGGGCACTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAAC 1654
                |  ||| | |   |||| |||||||| | |||||  ||   ||||||||  ||||
Db       1668 TTAGATGTGCCACGAAGGGCCCTTTGGTGGGCTGTGTGACAGTCGCGTGTGTCATGAAGT 1727

Qy       1655 GTGAAATAAAAAGAGCAAAAAAAAA 1679
              |||||||    ||    ||||||||
Db       1728 GTGAAATCTGGAGGAAGAAAAAAAA 1752


RESULT 3
BM807426
LOCUS       BM807426               1033 bp    mRNA    linear   EST 05-MAR-2002
DEFINITION  AGENCOURT_6581928 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5471935
            5', mRNA sequence.
ACCESSION   BM807426
VERSION     BM807426.1  GI:19124249
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1033)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1981  row: c  column: 08
            High quality sequence stop: 639.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5471935"
                     /tissue_type="amelanotic melanoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_41"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      291 a    266 c    264 g    212 t
ORIGIN

  Query Match           43.7%;  Score 733.4;  DB 12;  Length 1033;
  Best Local Similarity  92.5%;  Pred. No. 6.2e-94;
  Matches  830;  Conservative    0;  Mismatches   26;  Indels   41;  Gaps    4;

Qy        663 TTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAG 722
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAG 60

Qy        723 GGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCCGTGGTACGGAGAGTAAAGG 782
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCCGTGGTACGGAGAGTAAAGG 120

Qy        783 TCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGAC 842
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGAC 180

Qy        843 AAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACA 902
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACA 240

Qy        903 AGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCC 962
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Db        241 AGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCC 300

Qy        963 TCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGG 1022
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGG 360

Qy       1023 CCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTT---------------- 1066
              ||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGAAGTGAAAACTACAG 420

Qy       1067 ----------------GGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGA 1109
                             ||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCCTGACCCCTTGGAAAGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGA 480

Qy       1110 GGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGAT 1169
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGAT 540

Qy       1170 GTGAGTGCCACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGC 1229
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Db        541 GTGAGTGCCACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGC 600

Qy       1230 AATGGCAACACCGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGC 1289
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Db        601 AATGGCAACACCGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGC 660

Qy       1290 CTCATGGGACAGAAATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAAAGAGTTTT 1349
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Qy       1350 AAAAAAGAAATTGAAAATTGCCTTGCAGATATTTAGGTACAATGGAGTTTTCTTTTCCCA 1409
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Qy       1410 AACGGGAAGAACACAGCACACCC-GGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTC 1468
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Db        779 AACGGGAAGAACACAGCACACCCGGGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTC 838

Qy       1469 TTTGGTGCCAGTGTGGG-----CAAGGGCTCAGCCTCTCTGCCCACAGAGTGCCCCC 1520
              ||| | | |    ||||        ||| ||| |   ||||||||||| || ||||
Db        839 TTTTGGGGGCCAATGGGGGGCAAGGGGGTTCATCTCTTCTGCCCACAGAATGGCCCC 895
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RESULT 4
BM809227
LOCUS       BM809227                1083 bp    mRNA    linear   EST 05-MAR-2002
DEFINITION  AGENCOURT_6582414 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5468221
            5', mRNA sequence.
ACCESSION   BM809227
VERSION     BM809227.1  GI:19126050
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1083)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1971  row: h  column: 14
            High quality sequence stop: 656.
FEATURES             Location/Qualifiers
     source          1. .1083
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5468221"
                     /tissue_type="amelanotic melanoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_41"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling-Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      301 a    288 c    271 g    218 t      5 others
ORIGIN

  Query Match           42.9%;  Score 720.2;  DB 12;  Length 1083;
  Best Local Similarity   91.7%;  Pred. No. 4.4e-92;
  Matches  853;  Conservative    0;  Mismatches   34;  Indels   43;  Gaps    7;

Qy        663 TTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAG 722
              ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db          1 TTGGCTTTGTGAGTGATGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAG 60

Qy        723 GGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCCGTGGTACGGAGAGTAAAGG 782
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGG 120

Qy        783 TCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGAC 842
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGAC 180

Qy        843 AAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACA 902
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Db        181 AAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACA 240

Qy        903 AGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCC 962
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Db        241 AGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCC 300

Qy        963 TCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGG 1022
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Db        301 TCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGG 360

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Qy       1067 ----------------GGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGA 1109
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Db        421 CCCTGACCCCTTGGAAAGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGA 480

Qy       1110 GGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGAT 1169
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Db        481 GGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGAT 540

Qy       1170 GTGAGTGCCACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGC 1229
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Db        541 GTGAGTGCCACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGC 600

Qy       1230 AATGGCAACACCGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGC 1289
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AATGGCAACACCGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGC 660

Qy       1290 CTCATGGGACAGAAATTTGAGGGAGGGGAACAAAGAATACTTT-GGGGGGAAAAGAGTTT 1348
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Db        661 CTCATGGGACAGAAATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGGAAAAGAGTTT 720

Qy       1349 TAAAAAAGAAATTGAAAATTG-CCTTGCAGATATTTAGGTACAATGGAGTTTTCTTTTCC 1407
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Db        721 TAAAAAAGAAATTGAAAATTGCCCTTGCACATATTTAGGTACAATGGAGTTTTTCTTATT 780

Qy       1408 CAAACGGGAAGAACACAGCA----CACCCGGCTTGGACCCACTGCAAGCTGCATCGTGCA 1463
              | ||  | | ||  || ||      || ||||||||||||||||||||||||||||||
Db        781 CCAAAACGGAAAAANCACCAGCACACCCGGGCTTGGACCCACTGCAAGCTGCATCGTGCC 840

Qy       1464 ACCTCTTTGGTGCCAGTGTGGG-CAAGGGCTCAGCC-TCTCTGCCCACAGAGTGCCCCCA 1521
              |||   |||||||||||||||| |||||||||||| |||||||||||||| || |||||
Db        841 ACCCTCTTGGTGCCAGTGTGGGCCAAGGGCTCAGCCTTCTCTGCCCACAGAATGGCCCCA 900

Qy       1522 --CGTGGAACATTCTGGAGCTGGCCATCCC 1549
                | |||||||||| |||| |   ||
Db        901 ACGTGGAAACATTCTGGAACTGGGCCATCC 930


RESULT 5
BI666583
LOCUS       BI666583                865 bp    mRNA    linear   EST 12-SEP-2001
DEFINITION  603291469F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5310833 5',
            mRNA sequence.
ACCESSION   BI666583
VERSION     BI666583.1  GI:15580816
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 865)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11787  row: j  column: 18
            High quality sequence stop: 742.
FEATURES             Location/Qualifiers
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                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_96"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
                     ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3',
                     size-selected for  average insert size 2.3 kb and
                     normalized to ROT 5. This is a primary library enriched
                     for full-length  clones and constructed using the
                     Cap-trapper method (Carninci, in preparation).  Library
                     constructed by M. Brownstein (NIMH/NHGRI, National
                     Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT      250 a    230 c    209 g    176 t
ORIGIN

  Query Match             40.1%;  Score 674;  DB 12;  Length 865;
  Best Local Similarity   99.9%;  Pred. No. 1.5e-85;
  Matches  685;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60
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Qy         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 AAGAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 AAGAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 229

Qy        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCCGCAGCGGAGATGC 240
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Qy        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
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Qy        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        410 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 469

Qy        421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
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Db        470 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 529

Qy        481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540
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Db        530 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 589

Qy        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAAC-AATATTAGCCTCA 599
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Db        590 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAAATATTAGCCTCA 649

Qy        600 CCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAG 659
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Qy        660 CGGTTGGCTTTGTGAGTGAAGACGAA 685
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Db        710 CGGTTGGCTTTGTGAGTGAAGACGAA 735
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RESULT 6
BU155617
LOCUS       BU155617                856 bp    mRNA    linear   EST 03-SEP-2002
DEFINITION  AGENCOURT_7973225 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6166839
            5', mRNA sequence.
ACCESSION   BU155617
VERSION     BU155617.1  GI:22669149
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 856)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13527  row: m  column: 16
            High quality sequence stop: 593.
FEATURES             Location/Qualifiers
     source          1. .856
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6166839"
                     /tissue_type="melanotic melanoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_72"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 2 kb.   Library constructed by Life
                     Technologies."
BASE COUNT      217 a    228 c    239 g    172 t
ORIGIN

  Query Match             39.6%;  Score 664.8;  DB 13;  Length 856;
  Best Local Similarity   97.6%;  Pred. No. 2.9e-84;
  Matches  728;  Conservative    0;  Mismatches   12;  Indels    6;  Gaps    5;

Qy        214 AGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGT 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         94 AGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGT 153

Qy        274 CCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGC 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 CCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGC 213

Qy        334 CTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCG 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 CTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCG 273

Qy        394 CGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGT 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 CGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGT 333

Qy        454 GTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAG 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 GTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAG 393

Qy        514 GGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCAT 573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 GGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCAT 453

Qy        574 TAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGT 633
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        454 TAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGT 513

Qy        634 TACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGA 693
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 TACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGA 573

Qy        694 AATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGT 753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 AATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGT 633

Qy        754 GGCCGCGCCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGA 813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 GGCCGCGCCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGA 693

Qy        814 AGCCAAGGGTACAGGTGT-CCCCGTGGGACAAAAGGGGACACTGCAG-TGTGAAGCCTCA 871
              |||||||||||||||||| |||||||||||||||||||||||||| |||||| |||||
Db        694 AGCCAAGGGTACAGGTGTCCCCCGTGGGACAAAAGGGGACACTGCAGTTGTGAAACCTCA 753

Qy        872 GCAGTCCCCTCAGCAG-AATTCCAGTGGTACAAGGATG-ACAAAAGACTGATT--GAAGG 927
              |||||||||||||||| |||||||||||||||| |||||- || |||||||||||   | ||
Db        754 GCAGTCCCCTCAGCAGAAATTCCAGTGGTACAGGGATGAACCAAAGACTGATTTGAAGGG 813

Qy        928 AAAGAAAGGGGTGAAAGTGGAAAACA 953
              ||| |||||||||| ||  ||  || |
Db        814 AAAAAAAGGGGTGGAAAGGGGGAAAA 839


RESULT 7
AL533026
LOCUS       AL533026               1085 bp    mRNA    linear   EST 23-MAY-2003
DEFINITION  AL533026 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
            CS0DN005YD20 5-PRIME, mRNA sequence.
ACCESSION   AL533026
VERSION     AL533026.2  GI:31070858
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1085)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
COMMENT     On Feb 13, 2001 this sequence version replaced gi:12796519.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 6387.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DN005DB10QP1&cluster=6387.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DN005DB10QP1.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DN005YD20"
                     /tissue_type="ADULT BRAIN"
                     /dev_stage="adult"
                     /clone_lib="Homo sapiens ADULT BRAIN"
                     /note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-strand cDNA was digested with Not I and
                     cloned into the Not I and EcoRV sites of the pCMVSPORT 6
                     vector. Library was not normalized."
BASE COUNT      318 a    261 c    263 g    234 t      9 others
ORIGIN
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  Query Match          38.4%;  Score 645;  DB 9;  Length 1085;
  Best Local Similarity   86.8%;  Pred. No. 1.6e-81;
  Matches  806;  Conservative    1;  Mismatches    1;  Indels  121;  Gaps    4;

Qy        531 AAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATA 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        160 AAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATA 219

Qy        591 TTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCT 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 TTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCT 279

Qy        651 CTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCC 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 CTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCC 339

Qy        711 GGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCCGTGGTAC 770
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 GGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCCGTGGTAC 399

Qy        771 GGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTG 830
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        400 GGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTG 459

Qy        831 TCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAAT 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        460 TCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAAT 519

Qy        891 TCCAGTGGTACAAGGATGACAAAA---------------------------------- 914
              ||||||||||||||||||||||||
Db        520 TCCAGTGGTACAAGGATGACAAAAGAGCTGAAATCTCATTCACAGTTTGGTTATGATGGG 579

Qy        915 ---------------------------------------------------------- 914

Db        580 AAAGCTTCCTCCCCATGGTGGACGAATGGTGTCAAAACGGCCAGTGGGATCAATCAGCCT 639

Qy        915 ----------------------GACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAAC 952
                                     ||||||||||||||||||||||||||||||||||||||
Db        640 GACTTGCTCGCAGAATCCTCCCGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAAC 699

Qy        953 AGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTAC 1012
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        700 AGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTAC 759

Qy       1013 ACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCA 1072
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        760 ACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCA 819

Qy       1073 GGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTG 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        820 GGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTG 879

Qy       1133 CCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGG 1192
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        880 CCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGT-SCACTTCCCCACCCGG 938

Qy       1193 GAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCA 1252
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        939 GAAAGGCTGCCGCCACCACCACCACCAACACAACAGC-ATGGCAACACCGACAGCAACCA 997

Qy       1253 ATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGG 1312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        998 ATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGG 1057

Qy       1313 AGGGGAACAAAGAATACTTTGGGGGGAAA 1341
              ||||| |||||||||||||||||| |||
Db       1058 AGGGG-ACAAAGAATACTTTGGGGGAAAA 1085


RESULT 8
BI551784
LOCUS       BI551784               732 bp    mRNA    linear   EST 05-SEP-2001
DEFINITION  603197479F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5277115 5',
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            mRNA sequence.
ACCESSION   BI551784
VERSION     BI551784.1  GI:15439096
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 732)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11699  row: m  column: 20
            High quality sequence stop: 732.
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                     /clone="IMAGE:5277115"
                     /tissue_type="hippocampus"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_95"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
                     ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTVN-3',
                     size-selected for  average insert size 2.5 kb and
                     normalized to ROT 5. This is a primary library enriched
                     for  full-length clones and constructed using the
                     Cap-trapper method (Carninci, in preparation).  Library
                     constructed by M. Brownstein (NIMH/NHGRI, National
                     Institutes of Health).  Note: this is a NIH_MGC Library."
BASE COUNT      218 a    191 c    172 g    150 t      1 others
ORIGIN
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Query Match 38.3%; Score 643; DB 12; Length 732;
Best Local Similarity 99.4%; Pred. No. 3.6e-81;
Matches 676; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

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Qy          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         54 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 113

Qy         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAA-AAAGAA 119
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        114 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAACAAAGAA 173

Qy        120 GAAGAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAA 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        174 GAAGAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAA 233

Qy        180 TCTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATG 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 TCTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATG 293

Qy        240 CCACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCA 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        294 CCACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCA 353

Qy        300 GGTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCT 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 GGTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCT 413

Qy        360 ATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAA 419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 ATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAA 473

Qy        420 CGCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCT 479
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 CGCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCT 533

Qy        480 CGGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTC 539
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        534 CGGTGCAGACAGACAANCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTC 593

Qy        540 CCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCA 599
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        594 CCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCA 653

Qy        600 CCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGG-AGACACATCTCTCCCAAA 658
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        654 CCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAAGACACATCTCTCCCAAA 713

Qy        659 GCGGTTGGCTTTGTGAGTGA 678
              |||| ||||||||||||||||
Db        714 GCGG-TGGCTTTGTGAGTGA 732
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RESULT 9
BE798585
LOCUS       BE798585               1039 bp    mRNA    linear   EST 20-SEP-2000
DEFINITION  601581610F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935955 5',
            mRNA sequence.
ACCESSION   BE798585
VERSION     BE798585.1  GI:10219783
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1039)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM779  row: d  column: 04
            High quality sequence stop: 849.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3935955"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT      274 a    271 c    286 g    207 t      1 others
ORIGIN
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Query Match 37.8%; Score 635.2; DB 10; Length 1039;

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  Best Local Similarity   97.6%;  Pred. No. 4e-80;
  Matches  656;  Conservative    0;  Mismatches   13;  Indels    3;  Gaps    1;

Qy        298 CAGGTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCT 357
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db         65 CAGGTGCACTATTGACAACCGGGTCGCCCGGGTGGCCTGGCTAAACCGCAGCACCATCCT 124

Qy        358 CTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCA 417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 CTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCA 184

Qy        418 AACGCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTG 477
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 AACGCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTG 244

Qy        478 CTCGGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATC 537
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 CTCGGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATC 304

Qy        538 TCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCT 597
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 TCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCT 364

Qy        598 CACCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAA 657
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        365 CACCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAA 424

Qy        658 AGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCA 717
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        425 AGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCA 484

Qy        718 GTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCCGTGGTACGGAGAGT 777
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        485 GTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCCGTGGTACGGAGAGT 544

Qy        778 AAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGT 837
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        545 AAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGT 604

Qy        838 GGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTG 897
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        605 GGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTG 664

Qy        898 GTACAAGGATGACAAAAGACTGATTGAAGGAA---AGAAAGGGGTGAAAGTGGAAAACAG 954
              |||||||||||||||||||||||||||||||   | |  || |   | ||||||||||
Db        665 GTACAAGGATGACAAAAGACTGATTGAAGGAACAGACAGGGGTGAACAGTTGGAAAACAG 724

Qy        955 ACCTTTCCTCTC 966
              ||||||   |||
Db        725 ACCTTTTTCCTC 736


RESULT 10
BI549918
LOCUS       BI549918                 784 bp    mRNA    linear   EST 05-SEP-2001
DEFINITION  603194765F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5274161 5',
            mRNA sequence.
ACCESSION   BI549918
VERSION     BI549918.1  GI:15437230
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 784)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
            cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11692  row: b  column: 18
            High quality sequence stop: 726.
FEATURES             Location/Qualifiers
     source          1..784
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5274161"
                     /tissue_type="hippocampus"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_95"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
                     ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3',
                     size-selected for  average insert size 2.5 kb and
                     normalized to ROT 5. This is a primary library enriched
                     for  full-length clones and constructed using the
                     Cap-trapper method (Carninci, in preparation).  Library
                     constructed by M. Brownstein (NIMH/NHGRI, National
                     Institutes of Health).  Note: this is a NIH_MGC Library."
BASE COUNT      234 a    211 c    184 g    155 t
ORIGIN

  Query Match           37.4%;  Score 628.4;  DB 12;  Length 784;
  Best Local Similarity   98.4%;  Pred. No. 3.9e-79;
  Matches  667;  Conservative    0;  Mismatches    6;  Indels    5;  Gaps    3;

Qy          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 119

Qy         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 179

Qy        121 AAGAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 AAGAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 239

Qy        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 299

Qy        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 359

Qy        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 419

Qy        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 479

Qy        421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 539

Qy        481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 599

Qy        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCA- 599
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 CAAAA-TGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 658

Qy        600 CCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACAC---ATCTCTCCCA 656
```

```
Db        659 CCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACCATCTCCCCCCAA 718

Qy        657 AAGCGGTTGGCTTTGTGA 674
              ||||||||||||||| | ||
Db        719 AAGCGGTTGGCTTCGCGA 736


RESULT 11
BI913885
LOCUS       BI913885                870 bp    mRNA    linear   EST 16-OCT-2001
DEFINITION  603183295F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5247550 5',
            mRNA sequence.
ACCESSION   BI913885
VERSION     BI913885.1  GI:16178206
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 870)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11624  row: m  column: 23
            High quality sequence stop: 737.
FEATURES             Location/Qualifiers
     source          1..870
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5247550"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_121"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks.  Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     0.7-3.5 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics  tracking code 017. Note:
                     this is a NIH_MGC Library."
BASE COUNT      280 a    200 c    213 g    177 t
ORIGIN

  Query Match           37.0%;  Score 621.2;  DB 12;  Length 870;
  Best Local Similarity   99.4%;  Pred. No. 3.9e-78;
  Matches  634;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy       1042 CACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCAC 1101
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCAC 60

Qy       1102 GTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAA 1161
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAA 120

Qy       1162 ATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAAC 1221
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 A-TTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAAC 179

Qy       1222 ACAACAGCAATGGCAACACCGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGA 1281
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 ACAACAGCAATGGCAACACCGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGA 239

Qy       1282 AACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAA 1341
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 AACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAA 299

Qy       1342 AGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATATTTAGGTACAATGGAGTTTTC 1401
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 AAAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATATTTAGGTACAATGGAGTTTTC 359

Qy       1402 TTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGACCCACTGCAAGCTGCATCGTG 1461
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 TTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGACCCACTGCAAGCTGCATCGTG 419

Qy       1462 CAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTCTCTGCCCACAGAGTGCCCCCA 1521
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 CAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTCTCTGCCCACAGAGTGCCCCCA 479

Qy       1522 CGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCAGTCCATAGAGACGAACAGAAT 1581
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 CGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCAGTCCATAGAGACGAACAGAAT 539

Qy       1582 GAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTGGTAGACTGTGCCACCACGGCG 1641
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 GAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTGGTAGACTGTGCCACCACGGCG 599

Qy       1642 TGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
              |||||||||||||||||||||||||||||| ||| ||
Db        600 TGTGTTGTGAAACGTGAAATAAAAAGAGCAAGAAAGAA 637


RESULT 12
CD354474
LOCUS       CD354474                765 bp    mRNA    linear   EST 29-MAY-2003
DEFINITION  UI-M-GM0-cgd-g-16-0-UI.r1 NIH_BMAP_GM0 Mus musculus cDNA clone
            IMAGE: 30361215 5', mRNA sequence.
ACCESSION   CD354474
VERSION     CD354474.1  GI:31146975
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 765)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jim Lin, University of Iowa
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/mousefl.html
            This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
            Seq primer: pYX-5.
FEATURES             Location/Qualifiers
     source          1..765
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="IMAGE: 30361215"
                     /tissue_type="whole brain"
                     /dev_stage="1, 5 and 15 days newborn"
                     /lab_host="DH10B (T1 phage resistant)"
                     /clone_lib="NIH_BMAP_GM0"
                     /note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
                     Site_2: Not I; The library was constructed according
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
```

1996. Denatured RNA was size fractionated on a 1% agarose gel.First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site.Double strand cDNA was size selected according to mRNA size fraction,ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGAACTGAAT. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

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BASE COUNT      197 a    204 c    206 g    156 t      2 others
ORIGIN

  Query Match           36.9%;  Score 619.6;  DB 14;  Length 765;
  Best Local Similarity   91.0%;  Pred. No. 6.8e-78;
  Matches  658;  Conservative    0;  Mismatches   65;  Indels    0;  Gaps    0;

Qy        148 GCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTGGCTGCTCTGTGTCT 207
              | ||||||||||||||||||||||| |||||||||||||||||||||||| |||||||| ||
Db          1 GGCAAAAATGCACAATTCTATCTCGTGGGCAATCTTCACGGGGCTGGCGGCTCTGTGCCT 60

Qy        208 CTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGT 267
              ||||||||||||||| ||||| |||||||||||||||| ||||||||||||||||||||
Db         61 CTTCCAAGGAGTGCCGGTGCGTAGCGGAGATGCCACCTTTCCCAAAGCTATGGACAACGT 120

Qy        268 GACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCG 327
              ||||||| |||||||||||||||||||||||||||||| |||||||||| ||||||||
Db        121 GACGGTCAGGCAGGGGGAGAGCGCCACCCTCAGGTGCACAATTGACAACCGAGTCACCCG 180

Qy        328 GGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGA 387
              |||||||||||||||||||| |||||||||||||||.|||||||||||||||||| ||
Db        181 GGTGGCCTGGCTAAACCGCAGTACCATCCTCTATGCTGGAAATGACAAGTGGTGCCTAGA 240

Qy        388 TCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGT 447
              |||||| |||||||| ||||| |||||||| || |||||||||| |||||||||| ||
Db        241 TCCTCGTGTGGTCCTCCTGAGTAACACCCAGACCCAGTACAGCATTGAGATCCAGAATGT 300

Qy        448 GGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGAC 507
              ||||||||| || |||||||||| |||||||||||||||||||||||||||||| |||||
Db        301 GGATGTGTACGATGAGGGCCCTTATACCTGCTCGGTACAGACAGACAACCACCCTAAGAC 360

Qy        508 CTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATAT 567
              ||| |||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        361 CTCCAGGGTCCACCTCATTGTACAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATAT 420

Qy        568 CTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCC 627
              |||||||||||||||||||| || |||||||| |||||||| || |||||||| |||||
Db        421 CTCCATTAATGAAGGGAACAACATCAGCCTCACTTGCATAGCCACAGGTAGACCGGAGCC 480

Qy        628 TACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATA 687
              ||| || || |||||||| || |||||||| || |||||||||||||||| || || ||
Db        481 TACAGTAACCTGGAGACATATTTCTCCCAAGGCCGTTGGCTTTGTGAGTGAGGATGAGTA 540

Qy        688 CTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAA 747
              | |||| || |||||||||||| ||||| |||||||| || |||||||||| ||||||||
Db        541 CCTGGAGATCCAGGGCATCACTCGGGAACAGTCAGGCGAGTACGAGTGCAGCGCCTCCAA 600

Qy        748 TGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACAT 807
              |||||||| || || |||||||| ||||| ||||||||||||||||||||||||||||||
Db        601 CGACGTGGCGGCACCAGTGGTACGAAGAGTGAAGGTCACCGTGAACTATCCACCATACAT 660

Qy        808 TTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGC 867
              |||||||| ||||| ||| |||||||||||||| || |||||||| ||||||||||||||
Db        661 CTCAGAAGCTAAGGGCACANGTGTCCCCGTGGGGCAGAAGGGGACTCTGCAGTGTGAAGC 720

Qy        868 CTC 870
              ||
Db        721 TTC 723
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RESULT 13

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BM679797/c
LOCUS       BM679797                737 bp    mRNA    linear   EST 27-FEB-2002
DEFINITION  UI-E-EJ0-ain-k-01-0-UI.s1 UI-E-EJ0 Homo sapiens cDNA clone
            UI-E-EJ0-ain-k-01-0-UI 3', mRNA sequence.
ACCESSION   BM679797
VERSION     BM679797.1  GI:18989693
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 737)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road , 4156  MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            Tissue Procurement: Dr. Gregg Hageman
             cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1..737
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-E-EJ0-ain-k-01-0-UI"
                     /tissue_type="fetal eyes, lens, eye anterior segment,
                     optic nerve, retina, Retina Foveal and Macular, RPE and
                     Choroid"
                     /dev_stage="fetal and adult"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone_lib="UI-E-EJ0"
                     /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-E-EJ0 is a subtracted cDNA library constructed
                     according to Bonaldo, Lennon and Soares, Genome Research,
                     6:791-806, 1996. First strand cDNA synthesis was primed
                     with an oligo-dT primer containing a Not I site. Double
                     stranded cDNA was ligated to an EcoR I adaptor, digested
                     with Not I, and cloned directionally into pT7T3-Pac
                     vector. The oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tags for this library are: fetal eyes, AGAATCAAGA
                     ; lens, CGATTAGCGA; eye anterior segment, AATGCCGCAT;
                     optic nerve, CCATTAAGTG; retina, CCGCG; Retina Foveal and
                     Macular, GTCC; RPE and Choroid, ACCTA. This library was
                     created for the program, Gene Discovery in the Visual
                     System, supported by National Eye Institute (NEI).
                     TAG_LIB=UI-E-EJ0
                     TAG_TISSUE=human fetal eyes
                     TAG_SEQ=AGAATCAAGA"
BASE COUNT      144 a    179 c    193 g    221 t
ORIGIN

  Query Match           36.4%;  Score 611;  DB 12;  Length 737;
  Best Local Similarity   94.4%;  Pred. No. 1.1e-76;
  Matches  690;  Conservative    0;  Mismatches    5;  Indels   36;  Gaps    4;

Qy        983 AATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCAC 1042
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Db        737 AATGTCTCTGAACATGACTAT-GGAACTACACTTGCGT-GCCTCCAACAAGCTGGGCCAC 680

Qy       1043 ACCAATGCCAGCATCATGCTATTT--------------------------------GGT 1069
              |||||| |||||||||||||||| |                                |||
Db        679 ACCAATTCCAGCATCATGCTATCTGAAGTGAAAACTACAGCCCTGACCCCTTGGAAAGGT 620

Qy       1070 CCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTG 1129
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 CCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTG 560

Qy       1130 CTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACC 1189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 CTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACC 500

Qy       1190 CGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAA 1249
              ||||||||| ||||||||||||||||||||||||||| ||||||||||||||||||||
Db        499 CGGGAAAGGATGCCGCCACCACCACCACCAACACAACAGCATTGGCAACACCGACAGCAA 440

Qy       1250 CCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGA 1309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 CCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGA 380

Qy       1310 GGGAGGGGAACAAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTG 1369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 GGGAGGGGAACAAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTG 320

Qy       1370 CCTTGCAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACA 1429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 CCTTGCAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACA 260

Qy       1430 CCCGGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAG 1489
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 CCCGGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAG 200

Qy       1490 GGCTCAGCCTCTCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCC 1549
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 GGCTCAGCCTCTCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCC 140

Qy       1550 AAATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTG 1609
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 AAATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTG 80

Qy       1610 CGGGCACTTTGGTAGACTGTGCCA-CCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGA 1668
              |||||||||||||||||||||||| |||||||||||||||||||||||| ||||||||
Db         79 CGGGCACTTTGGTAGACTGTGCCACCCACGGCGTGTGTTGTGAAACGTGAACTAAAAAGA 20

Qy       1669 GCAAAAAAAAA 1679
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Db         19 GCAAAAAAAAA 9
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RESULT 14
AW025115/c
LOCUS       AW025115               604 bp    mRNA    linear   EST 09-MAR-2000
DEFINITION  wu71h04.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:2525527 3'
            similar to SW:NTRI_RAT Q62718 NEUROTRIMIN PRECURSOR ;, mRNA
            sequence.
ACCESSION   AW025115
VERSION     AW025115.1  GI:5878645
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 604)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 1662    Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 465.
FEATURES             Location/Qualifiers
     source          1..604
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2525527"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Kid3"
                     /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer,
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not
                     I and Eco RI sites of the modified pT7T3 vector. mRNA
                     source: 2 pooled kidneys. Library went through one round
                     of normalization. Library constructed by Bento Soares and
                     M. Fatima Bonaldo. "
BASE COUNT      118 a    158 c    157 g    171 t
ORIGIN
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Query Match 35.9%; Score 602.4; DB 9; Length 604;
Best Local Similarity 99.8%; Pred. No. 1.9e-75;
Matches 603; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       1067 GGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGG 1126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 GGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGG 545

Qy       1127 CTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCC 1186
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        544 CTGCTGCCTCTTCTGGTCTTGCACATGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCC 485

Qy       1187 ACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAG 1246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 ACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAG 425

Qy       1247 CAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATT 1306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 CAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATT 365

Qy       1307 TGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAA 1366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAA 305

Qy       1367 TTGCCTTGCAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGC 1426
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Db        304 TTGCCTTGCAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGC 245

Qy       1427 ACACCCGGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGC 1486
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Db        244 ACACCCGGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGC 185

Qy       1487 AAGGGCTCAGCCTCTCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCAT 1546
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Db        184 AAGGGCTCAGCCTCTCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCAT 125

Qy       1547 CCCAAATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCG 1606
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Db        124 CCCAAATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCG 65

Qy       1607 CTGCGGGCACTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAA 1666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 CTGCGGGCACTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAA 5
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Qy       1667 GAGC 1670
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Db          4 GAGC 1


RESULT 15
BU741589/c
LOCUS       BU741589                602 bp    mRNA    linear   EST 10-OCT-2002
DEFINITION  UI-E-EO1-aiz-c-15-0-UI.s1 UI-E-EO1 Homo sapiens cDNA clone
            UI-E-EO1-aiz-c-15-0-UI 3', mRNA sequence.
ACCESSION   BU741589
VERSION     BU741589.1  GI:23687034
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 602)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road , 4156  MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            Tissue Procurement: Dr. Gregg Hageman
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .602
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-E-EO1-aiz-c-15-0-UI"
                     /tissue_type="fetal eye"
                     /dev_stage="fetal"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone_lib="UI-E-EO1"
                     /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-E-EO1 is a normalized cDNA library containing the
                     following tissue(s): fetal eye. The library was
                     constructed according to Bonaldo, Lennon and Soares,
                     Genome Research, 6:791-806, 1996. First strand cDNA
                     synthesis was primed with an oligo-dT primer containing a
                     Not I site. Double stranded cDNA was ligated to an EcoR I
                     adaptor, digested with Not I, and cloned directionally
                     into pT7T3-Pac vector. The oligonucleotide used to prime
                     the synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     CGCGTATACC. This library was created for the program, Gene
                     Discovery in the Visual System, supported by National Eye
                     Institute (NEI).
                     TAG_LIB=UI-E-EO1
                     TAG_TISSUE=human fetal eye
                     TAG_SEQ=CGCGTATACC"
BASE COUNT      117 a    154 c    155 g    176 t
ORIGIN

  Query Match           35.7%;  Score 598.8;  DB 13;  Length 602;
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  Best Local Similarity   99.7%;  Pred. No. 6.2e-75;
  Matches  600;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1074 GCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGC 1133
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       602 GCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGC 543

Qy      1134 CTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGG 1193
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       542 CTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGG 483

Qy      1194 AAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAA 1253
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Db       482 AAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAA 423

Qy      1254 TCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGA 1313
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       422 TCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGA 363

Qy      1314 GGGGAACAAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTT 1373
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      1374 GCAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCG 1433
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Db       302 GCAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCG 243

Qy      1434 GCTTGGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCT 1493
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       242 GCTTGGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCT 183

Qy      1494 CAGCCTCTCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAAT 1553
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Db       182 CAGCCTCTCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAAT 123

Qy      1554 TCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGG 1613
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       122 TCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGG 63

Qy      1614 CACTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAA 1673
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db         62 CACTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAAAAAA 3

Qy      1674 AA 1675
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Db          2 AA 1


Search completed: September 11, 2003, 02:49:02
Job time : 4341 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 10, 2003, 22:48:16 ; Search time 570 Seconds
(without alignments)
7951.503 Million cell updates/sec

Title: US-10-017-084A-522
Perfect score: 1679
Sequence: 1 gttgtgtccttcagcaaaac.....ataaaaagagcaaaaaaaaa 1679

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1679	100.0	1679	20	AAZ34324	Human PRO337 nucle
2	1679	100.0	1679	21	AAC78590	Human PRO337 nucle
3	1679	100.0	1679	22	AAS21431	Human cDNA sequenc
4	1679	100.0	1679	22	AAC87037	Nucleotide sequenc
5	1679	100.0	1679	24	ABL95588	Human angiogenesis
6	1679	100.0	1679	24	ABL88099	Human PRO337 cDNA
7	1679	100.0	1679	24	ABK33598	cDNA encoding huma
8	1679	100.0	1679	25	ACA60526	Novel human secret
9	1679	100.0	1679	25	ACA03790	cDNA encoding huma
10	1679	100.0	1679	25	ACA04211	Human cDNA encodin
11	1679	100.0	1679	25	ACA04516	Novel human secret
12	1679	100.0	1679	25	ACA04996	Novel human secret
13	1679	100.0	1679	25	ABX89328	DNA encoding novel
14	1679	100.0	1679	25	ABX92696	cDNA encoding huma
15	1661.4	99.0	1693	21	AAZ47893	Human protein enco
16	1643.4	97.9	2012	21	AAA88791	Human SECX cDNA Cl
17	1601.4	95.4	1603	21	AAA88790	Human SECX cDNA Cl
18	1509.8	89.9	1873	24	ABK49272	Human Kruppel asso
19	1457	86.8	1678	22	AAI57869	Human polynucleoti
20	1432.8	85.3	1839	25	ABX76448	Lung cancer-associ
21	1315	78.3	1690	22	AAI59655	Human polynucleoti
22	1032	61.5	1032	21	AAZ47892	Human protein enco
23	939	55.9	939	21	AAZ47894	Human protein enco
24	803.8	47.9	832	21	AAA44536	Human secreted exp
25	540.8	32.2	3069	14	AAQ51015	Rat opioid recepto
26	523	31.1	2179	14	AAQ51017	Rat opioid recepto
27	523	31.1	2337	14	AAQ51016	Rat opioid recepto
28	503	30.0	503	20	AAZ34325	Human EST DNA42301
29	503	30.0	503	21	AAC78591	Human EST DNA42301
30	503	30.0	503	25	ABX92697	Human PRO337 EST p
31	491.2	29.3	537	22	AAC91321	Human polynucleoti
32	441.2	26.3	452	22	AAF93346	Spinal cord tissue
33	396	23.6	484	23	AAS78035	DNA encoding novel
34	343.8	20.5	1411	24	AAL50356	Human limbic syste
35	343	20.4	1238	17	AAT42080	Rat LAMP coding se
36	341.6	20.3	1195	25	ABX63560	Human cDNA #560 di
37	340.6	20.3	924	17	AAT42084	Human LAMP residue
38	340.6	20.3	977	17	AAT42079	Human LAMP residue
39	340.6	20.3	1014	17	AAT42081	Rat LAMP coding se
40	338.6	20.2	861	17	AAT42086	Human LAMP residue
41	338.6	20.2	912	17	AAT42082	Human mature LAMP
42	337.4	20.1	945	17	AAT42085	Rat LAMP residues
43	337.4	20.1	1757	25	ABZ76264	Human GENSET cDNA
44	337	20.1	930	17	AAT42083	Rat mature LAMP co
45	333.8	19.9	861	17	AAT42087	Rat LAMP residues

ALIGNMENTS

RESULT 1
AAZ34324
ID AAZ34324 standard; cDNA; 1679 BP.
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AC AAZ34324;
XX
DT 07-DEC-1999 (first entry)
XX
DE Human PRO337 nucleotide sequence.
XX
KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein; ss.
XX
OS Homo sapiens.
XX
PN WO9946281-A2.
XX
PD 16-SEP-1999.
XX
PF 08-MAR-1999; 99WO-US05028.
XX
PR 10-MAR-1998; 98US-0077450.
PR 11-MAR-1998; 98US-0077632.
PR 11-MAR-1998; 98US-0077641.
PR 11-MAR-1998; 98US-0077649.
PR 12-MAR-1998; 98US-0077791.
PR 13-MAR-1998; 98US-0078004.
PR 17-MAR-1998; 98US-0040220.
PR 20-MAR-1998; 98US-0078886.
PR 20-MAR-1998; 98US-0078910.

PR 20-MAR-1998; 98US-0078936.
PR 20-MAR-1998; 98US-0078939.
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PR 26-MAR-1998; 98US-0079656.
PR 27-MAR-1998; 98US-0079663.
PR 27-MAR-1998; 98US-0079664.
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PR 30-MAR-1998; 98US-0079920.
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PR 31-MAR-1998; 98US-0080105.
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PR 31-MAR-1998; 98US-0080194.
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PR 08-APR-1998; 98US-0081049.
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PR 09-APR-1998; 98US-0081195.
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PR 15-APR-1998; 98US-0081838.
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PR 21-APR-1998; 98US-0082568.
PR 21-APR-1998; 98US-0082569.
PR 22-APR-1998; 98US-0082700.
PR 22-APR-1998; 98US-0082704.
PR 22-APR-1998; 98US-0082804.
PR 23-APR-1998; 98US-0082767.
PR 23-APR-1998; 98US-0082796.
PR 27-APR-1998; 98US-0083336.
PR 28-APR-1998; 98US-0083322.
PR 29-APR-1998; 98US-0083392.
PR 29-APR-1998; 98US-0083495.
PR 29-APR-1998; 98US-0083496.
PR 29-APR-1998; 98US-0083499.
PR 29-APR-1998; 98US-0083500.
PR 29-APR-1998; 98US-0083545.
PR 29-APR-1998; 98US-0083554.
PR 29-APR-1998; 98US-0083558.
PR 29-APR-1998; 98US-0083559.
PR 30-APR-1998; 98US-0083742.
PR 05-MAY-1998; 98US-0084366.
PR 06-MAY-1998; 98US-0084414.
PR 06-MAY-1998; 98US-0084441.
PR 07-MAY-1998; 98US-0084598.
PR 07-MAY-1998; 98US-0084600.
PR 07-MAY-1998; 98US-0084627.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084639.
PR 07-MAY-1998; 98US-0084640.
PR 07-MAY-1998; 98US-0084643.
PR 13-MAY-1998; 98US-0085323.
PR 13-MAY-1998; 98US-0085338.
PR 13-MAY-1998; 98US-0085339.
PR 15-MAY-1998; 98US-0085573.
PR 15-MAY-1998; 98US-0085579.
PR 15-MAY-1998; 98US-0085580.
PR 15-MAY-1998; 98US-0085582.
PR 15-MAY-1998; 98US-0085689.
PR 15-MAY-1998; 98US-0085697.
PR 15-MAY-1998; 98US-0085700.
PR 15-MAY-1998; 98US-0085704.
PR 18-MAY-1998; 98US-0086023.
PR 22-MAY-1998; 98US-0086392.
PR 22-MAY-1998; 98US-0086414.
PR 22-MAY-1998; 98US-0086430.
PR 22-MAY-1998; 98US-0086486.
PR 28-MAY-1998; 98US-0087098.
PR 28-MAY-1998; 98US-0087106.
PR 28-MAY-1998; 98US-0087208.
PR 30-JUL-1998; 98US-0094651.
PR 11-SEP-1998; 98US-0100038.
XX
PA (GETH) GENENTECH INC.
XX
PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX
DR WPI; 1999-551358/46.
DR P-PSDB; AAY41773.
XX
PT New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders -
XX
PS Claim 2; Fig 221; 530pp; English.
XX
CC The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as
CC sources of probes, primers, for chromosome mapping, and for generation
CC of antisense sequences. They can also be used to create transgenic
CC animals. The proteins can be used to treat a variety of diseases and
CC disorders, depending on their function. Diseases that may be treated
CC include blood coagulation disorders, cancers and cellular adhesion
CC disorders. They may also be used to raise antibodies. AAZ33891 to
CC AAZ34338, and AAY41685 to AAY41774 represent polynucleotide and
CC polypeptide sequence given in the exemplification of the present
CC invention.
XX
SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

Query Match 100.0%; Score 1679; DB 20; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60
Db 1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60

Qy 61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120
Db 61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120

Qy 121 AAGAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180
Db 121 AAGAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180

Qy 181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240
Db 181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240

Qy 241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300
Db 241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300

Qy 301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
Db 301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360

Qy 361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420
Db 361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420

Qy 421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
Db 421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480

Qy 481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540
Db 481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540

```
Qy       541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600

Qy       601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660

Qy       661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720

Qy       721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAA 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAA 780

Qy       781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840

Qy       841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900

Qy       901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960

Qy       961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020

Qy      1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080

Qy      1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140

Qy      1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200

Qy      1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260

Qy      1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320

Qy      1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380

Qy      1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440

Qy      1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500

Qy      1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560

Qy      1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620
```

```
Qy       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
```

RESULT 2
AAC78590
ID AAC78590 standard; cDNA; 1679 BP.
XX
AC AAC78590;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human PRO337 nucleotide sequence SEQ ID NO:522.
XX
KW Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
KW expressed sequence tag; detection; cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200053756-A2.
XX
PD 14-SEP-2000.
XX
PF 18-FEB-2000; 2000WO-US04341.
XX
PR 08-MAR-1999; 99WO-US05028.
PR 12-MAR-1999; 99US-0123957.
PR 29-MAR-1999; 99US-0126773.
PR 21-APR-1999; 99US-0130232.
PR 28-APR-1999; 99US-0131445.
PR 14-MAY-1999; 99US-0134287.
PR 23-JUN-1999; 99US-0141037.
PR 26-JUL-1999; 99US-0145698.
PR 29-OCT-1999; 99US-0162506.
PR 30-NOV-1999; 99WO-US28313.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2000-611443/58.
DR P-PSDB; AAB44329.
XX
PT Novel PRO polypeptides and polynucleotides used in detection methods,
PT to target bioactive molecules to specific cells, and to modulate
PT cellular activities -
XX
PS Claim 2; Fig 221; 636pp; English.
XX
CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed
CC sequence tag) sequences which encode secreted or transmembrane PRO
CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic
CC activity. The polynucleotides and polypeptides can be used for detecting
CC the presence of PRO polypeptides in samples, for linking bioactive
CC molecules to cells and for modulating biological activities of cells,
CC using the polypeptides for specific targeting. The polypeptide targeting
CC can be used to kill the target cells, e.g. for the treatment of cancers.
CC The polypeptide pairs provide specific targeting of bioactive molecules
CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
CC the isolation of the PRO polynucleotide sequences.

```
XX
SQ   Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

  Query Match           100.0%;  Score 1679;  DB 21;  Length 1679;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1679;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60

Qy         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120

Qy        121 AAGAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180

Qy        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240

Qy        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300

Qy        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360

Qy        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420

Qy        421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480

Qy        481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540

Qy        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600

Qy        601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660

Qy        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720

Qy        721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAA 780

Qy        781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840

Qy        841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900

Qy        901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960

Qy        961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020

Qy       1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080

Qy       1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140

Qy       1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200

Qy       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260

Qy       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320

Qy       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380

Qy       1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440

Qy       1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500

Qy       1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560

Qy       1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620

Qy       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679


RESULT 3
AAS21431
ID   AAS21431 standard; cDNA; 1679 BP.
XX
AC   AAS21431;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human cDNA sequence encoding for PRO337 polypeptide.
XX
KW   Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW   breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW   cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KW   adipocyte; A-peptide; factor VIIA; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO200140466-A2.
XX
PD   07-JUN-2001.
XX
PF   01-DEC-2000; 2000WO-US32678.
XX
PR   01-DEC-1999;   99WO-US28301.
PR   01-DEC-1999;   99WO-US28634.
PR   02-DEC-1999;   99WO-US28551.
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PR   02-DEC-1999;   99WO-US28564.
PR   02-DEC-1999;   99WO-US28565.
PR   09-DEC-1999;   99US-0170262.
PR   16-DEC-1999;   99WO-US30095.
PR   20-DEC-1999;   99WO-US30911.
PR   20-DEC-1999;   99WO-US30999.
PR   30-DEC-1999;   99WO-US31243.
PR   06-JAN-2000;  2000WO-US00277.
PR   06-JAN-2000;  2000WO-US00376.
PR   11-FEB-2000;  2000WO-US03565.
PR   18-FEB-2000;  2000WO-US04341.
PR   18-FEB-2000;  2000WO-US04342.
PR   22-FEB-2000;  2000WO-US04414.
PR   24-FEB-2000;  2000WO-US04914.
PR   24-FEB-2000;  2000WO-US05004.
PR   01-MAR-2000;  2000WO-US05601.
PR   20-MAR-2000;  2000WO-US07377.
PR   21-MAR-2000;  2000WO-US07532.
PR   30-MAR-2000;  2000WO-US08439.
PR   17-MAY-2000;  2000WO-US13705.
PR   22-MAY-2000;  2000WO-US14042.
PR   30-MAY-2000;  2000WO-US14941.
PR   02-JUN-2000;  2000WO-US15264.
PR   10-NOV-2000;  2000WO-US30873.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Beresini M,  Deforge L,  Desnoyers L,  Filvaroff E,  Gao W;
PI   Gerritsen ME,  Goddard A,  Godowski PJ,  Gurney AL,  Sherwood S;
PI   Smith V,  Stewart TA,  Tumas D,  Watanabe CK,  Wood WI,  Zhang Z;
XX
DR   WPI; 2001-408281/43.
DR   P-PSDB; AAU12359.
XX
PT   Isolated, secretory and transmembrane PRO polypeptide used to detect
PT   other PRO polypeptides, link bioactive molecules to cells expressing
PT   PRO polypeptides, and detect the presence of mammalian tumours e.g.
PT   lung, breast, prostate, cervical
XX
PS   Claim 3; Fig 375; 813pp; English.
XX
CC   AAS21244-AAS21518 encode for novel human secretory and transmembrane
CC   PRO polypeptides. The PRO polypeptides are useful to detect other
CC   PRO polypeptides, to link bioactive molecules to cells expressing
CC   PRO polypeptides, to modulate biological activities of cells expressing
CC   PRO polypeptides, and to detect the presence of mammalian lung, colon,
CC   breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC   polypeptide expression in a cell sample to that in a control sample.
CC   Some of the 275 sequences are also useful to stimulate the release of
CC   tumour necrosis factor-alpha (TNF-alpha) from human blood, the
CC   proliferation or differentiation of chondrocytes, the proliferation or
CC   gene expression in pericyte cells, the release of proteoglycans from
CC   cartilage, the proliferation of inner ear utricular supporting cells or
CC   of T-lymphocytes, the release of a cytokine from peripheral blood
CC   monocytes (PBMCs), or the proliferation of endothelial cells. Some of
CC   the PRO polypeptides may modulate glucose or free fatty acid uptake by
CC   skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
CC   to factor VIIA. The PRO polypeptides can be used in assays to identify
CC   molecules involved in binding interactions. The polynucleotides encoding
CC   PRO polypeptides can be used to generate probes, antisense RNA/DNA,
CC   transgenic or knock out animals and can be used in gene therapy.
XX
SQ   Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

  Query Match           100.0%;  Score 1679;  DB 22;  Length 1679;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1679;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60

Qy         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120

Qy        121 AAGAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180

Qy        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240

Qy        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300

Qy        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360

Qy        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420

Qy        421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480

Qy        481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540

Qy        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600

Qy        601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660

Qy        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720

Qy        721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAA 780

Qy        781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840

Qy        841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900

Qy        901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960

Qy        961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020

Qy       1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080

Qy       1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140

Qy       1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200

Qy      1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260

Qy      1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320

Qy      1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380

Qy      1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440

Qy      1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500

Qy      1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560

Qy      1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620

Qy      1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
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```
RESULT 4
AAC87037
ID   AAC87037 standard; cDNA; 1679 BP.
XX
AC   AAC87037;
XX
DT   20-APR-2001  (first entry)
XX
DE   Nucleotide sequence of human polypeptide PRO337.
XX
KW   Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;
KW   PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO1308;
KW   PRO1183; PRO1272; PRO1419; PRO4999; PRO7170; PRO248; PRO353; PRO1318;
KW   PRO1600; PRO9940; PRO533; PRO301; PRO187; PRO337; PRO1411; PRO4356;
KW   PRO246; PRO265; PRO941; PRO10096; PRO6003; PRO6004; PRO350; PRO2630;
KW   PRO6309; cell death; genetic disorder; transgenic animal; gene therapy;
KW   ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             134..1168
FT                   /*tag= a
FT   sig_peptide     134..216
FT                   /*tag= b
XX
PN   WO200077037-A2.
XX
PD   21-DEC-2000.
XX
PF   22-MAY-2000; 2000WO-US14042.
XX
PR   15-JUN-1999;   99US-0139695.
PR   20-JUL-1999;   99US-0145070.
PR   26-JUL-1999;   99US-0145698.
PR   17-AUG-1999;   99US-0149396.
PR   01-SEP-1999;   99WO-US20111.
PR   08-SEP-1999;   99WO-US20594.
PR   15-SEP-1999;   99WO-US21090.
PR   15-SEP-1999;   99WO-US21547.
PR   30-NOV-1999;   99WO-US28313.
PR   01-DEC-1999;   99WO-US28301.
PR   02-DEC-1999;   99WO-US28565.
PR   07-DEC-1999;   99US-0169495.
PR   05-JAN-2000; 2000WO-US00219.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   22-FEB-2000; 2000WO-US04414.
PR   01-MAR-2000; 2000WO-US05601.
PR   02-MAR-2000; 2000WO-US05841.
PR   20-MAR-2000; 2000WO-US07377.
PR   30-MAR-2000; 2000WO-US08439.
PR   15-MAY-2000; 2000WO-US13358.
PR   17-MAY-2000; 2000WO-US13705.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Botstein DA,  Desnoyers L,  Eaton DL;
PI   Ferrara N,  Fong S,  Gao W,  Gerber H,  Gerritsen ME,  Goddard A;
PI   Godowski PJ,  Gurney AL,  Kljavin IJ,  Mather JP,  Napier MA,  Pan J;
PI   Paoni NF,  Roy MA,  Stewart TA,  Tumas D,  Watanabe CK,  Williams PM;
PI   Wood WI,  Zhang Z;
XX
DR   WPI; 2001-050091/06.
DR   P-PSDB; AAB31204.
XX
PT   Isolated nucleic acid molecule encoding a PRO polypeptide which is a
PT   transmembrane polypeptide is useful for gene therapy and identification
PT   of related polypeptides -
XX
PS   Claim 2; Fig 51; 244pp; English.
XX
CC   The present sequence encodes a human secreted and transmembrane
CC   polypeptide. The specification describes human polypeptides, designated
CC   PRO196, PRO444, PRO183, PRO185, PRO210, PRO215, PRO217, PRO242, PRO288,
CC   PRO365, PRO1361, PRO1308, PRO1183, PRO1272, PRO1419, PRO4999, PRO7170,
CC   PRO248, PRO353, PRO1318, PRO1600, PRO9940, PRO533, PRO301, PRO187,
CC   PRO337, PRO1411, PRO4356, PRO246, PRO265, PRO941, PRO10096, PRO6003,
CC   PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of cells
CC   can be modulated with agents that bind to these polypeptides, resulting
CC   in the death of the cells. The polynucleotides encoding these
CC   polypeptides are useful in the recombinant production of the
CC   polypeptides, as a hybridisation probe to screen libraries to isolate
CC   homologous sequences, or to map the gene. They may also be used for
CC   analysing genetic disorders, and to produce transgenic animals which are
CC   useful for the development and screening of therapeutically useful
CC   reagents. The polynucleotides can also be used in gene therapy e.g. to
CC   replace a defective gene.
XX
SQ   Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

  Query Match          100.0%;  Score 1679;  DB 22;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1679;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60

Qy         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120

Qy        121 AAGAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180

Qy        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240
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Qy       241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300

Qy       301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360

Qy       361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420

Qy       421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480

Qy       481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540

Qy       541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600

Qy       601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660

Qy       661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720

Qy       721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCCGTGGTACGGAGAGTAAA 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCCGTGGTACGGAGAGTAAA 780

Qy       781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840

Qy       841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900

Qy       901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960

Qy       961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020

Qy      1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080

Qy      1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140

Qy      1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200

Qy      1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260

Qy      1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320

Qy      1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380

Qy      1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440

Qy      1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500

Qy      1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560

Qy      1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620

Qy      1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAAGAGCAAAAAAAAA 1679
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAAGAGCAAAAAAAAA 1679
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RESULT 5
ABL95588
ID ABL95588 standard; cDNA; 1679 BP.
XX
AC ABL95588;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human angiogenesis related cDNA PRO337 SEQ ID NO: 55.
XX
KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;
KW antiarteriosclerotic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200208284-A2.
XX
PD 31-JAN-2002.
XX
PF 09-JUL-2001; 2001WO-US21735.
XX
PR 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220664P.
PR 28-JUL-2000; 2000WO-US20710.
PR 02-AUG-2000; 2000US-222695P.
PR 17-AUG-2000; 2000US-0643657.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 07-SEP-2000; 2000US-230978P.
PR 15-SEP-2000; 2000US-000000P.
PR 18-SEP-2000; 2000US-0664610.
PR 18-SEP-2000; 2000US-0665350.
PR 24-OCT-2000; 2000US-242922P.
PR 08-NOV-2000; 2000US-0709238.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 22-JAN-2001; 2001US-0767609.
PR 28-FEB-2001; 2001US-0796498.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.

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PR   05-APR-2001; 2001US-0828366.
PR   10-MAY-2001; 2001US-0854208.
PR   10-MAY-2001; 2001US-0854280.
PR   25-MAY-2001; 2001US-0866028.
PR   25-MAY-2001; 2001US-0866034.
PR   25-MAY-2001; 2001WO-US17092.
PR   30-MAY-2001; 2001US-0870574.
PR   30-MAY-2001; 2001WO-US17443.
PR   01-JUN-2001; 2001WO-US17800.
PR   20-JUN-2001; 2001WO-US19692.
PR   28-JUN-2001; 2001WO-US00000.
XX
PA   (GETH ) GENENTECH INC.
PA   (BAKE/) BAKER K P.
PA   (FERR/) FERRARA N.
PA   (GERB/) GERBER H.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (HILL/) HILLAN K J.
PA   (MARS/) MARSTERS S A.
PA   (PANJ/) PAN J.
PA   (PAON/) PAONI N F.
PA   (STEP/) STEPHAN J F.
PA   (WATA/) WATANABE C K.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
XX
PI   Baker KP,  Ferrara N,  Gerber H,  Gerritsen ME,  Goddard A;
PI   Godowski PJ,  Gurney AL,  Hillan KJ,  Marsters SA,  Pan J,  Paoni NF;
PI   Stephan JF,  Watanabe CK,  Williams PM,  Wood WI,  Ye W;
XX
DR   WPI; 2002-171999/22.
DR   P-PSDB; ABB95450.
XX
PT   One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT   useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT   infarction), endothelial or angiogenic disorders in a mammal -
XX
PS   Claim 1; Fig 55; 567pp; English.
XX
CC   The present invention provides the protein and coding sequences of human
CC   PRO proteins. These are useful for treating or diagnosing a
CC   cardiovascular, endothelial or angiogenic disorder, including cardiac
CC   hypertrophy, trauma, cancer, age-related macular degeneration,
CC   atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC   angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC   angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC   healing. The present sequence is a coding sequence of the invention.
XX
SQ   Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

  Query Match           100.0%;  Score 1679;  DB 24;  Length 1679;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1679;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60

Qy         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120

Qy        121 AAGAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180

Qy        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240

Qy        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300

Qy        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360

Qy        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420

Qy        421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480

Qy        481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540

Qy        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600

Qy        601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660

Qy        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720

Qy        721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCCGTGGTACGGAGAGTAAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCCGTGGTACGGAGAGTAAA 780

Qy        781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840

Qy        841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900

Qy        901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960

Qy        961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020

Qy       1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080

Qy       1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140

Qy       1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200

Qy       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260

Qy       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320

Qy       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380

Qy       1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440

Qy       1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500

Qy       1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560

Qy       1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620

Qy       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679


RESULT 6
ABL88099
ID   ABL88099 standard; cDNA; 1679 BP.
XX
AC   ABL88099;
XX
DT   16-MAY-2002  (first entry)
XX
DE   Human PRO337 cDNA sequence SEQ ID NO:55.
XX
KW   Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
KW   vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW   gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KW   angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW   age-related macular degeneration; arterial restenosis; angina;
KW   rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW   lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW   wound healing; chromosome mapping; gene mapping; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200200690-A2.
XX
PD   03-JAN-2002.
XX
PF   20-JUN-2001; 2001WO-US19692.
XX
PR   23-JUN-2000; 2000US-213637P.
PR   20-JUL-2000; 2000US-219556P.
PR   25-JUL-2000; 2000US-220624P.
PR   25-JUL-2000; 2000US-220664P.
PR   28-JUL-2000; 2000WO-US20710.
PR   02-AUG-2000; 2000US-222695P.
PR   17-AUG-2000; 2000US-0643657.
PR   23-AUG-2000; 2000WO-US23522.
PR   24-AUG-2000; 2000WO-US23328.
PR   07-SEP-2000; 2000US-230978P.
PR   18-SEP-2000; 2000US-0664610.
PR   18-SEP-2000; 2000US-0665350.
PR   24-OCT-2000; 2000US-242922P.
PR   08-NOV-2000; 2000US-0709238.
PR   08-NOV-2000; 2000WO-US30952.
PR   10-NOV-2000; 2000WO-US30873.
PR   01-DEC-2000; 2000WO-US32678.
PR   20-DEC-2000; 2000US-0747259.
PR   20-DEC-2000; 2000WO-US34956.
PR   22-JAN-2001; 2001US-0767609.
PR   28-FEB-2001; 2001US-0796498.
PR   28-FEB-2001; 2001WO-US06520.
PR   01-MAR-2001; 2001WO-US06666.
PR   09-MAR-2001; 2001US-0802706.
PR   14-MAR-2001; 2001US-0808689.
PR   22-MAR-2001; 2001US-0816744.
PR   05-APR-2001; 2001US-0828366.
PR   10-MAY-2001; 2001US-0854208.
PR   10-MAY-2001; 2001US-0854280.
PR   25-MAY-2001; 2001US-0866028.
PR   25-MAY-2001; 2001US-0866034.
PR   25-MAY-2001; 2001WO-US17092.
PR   30-MAY-2001; 2001US-0870574.
PR   30-MAY-2001; 2001WO-US17443.
PR   01-JUN-2001; 2001WO-US17800.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Ferrara N,  Gerber H,  Gerritsen ME,  Goddard A;
PI   Godowski PJ,  Gurney AL,  Hillan KJ,  Marsters SA,  Pan J,  Paoni NF;
PI   Stephan JF,  Watanabe CK,  Williams PM,  Wood WI,  Ye W;
XX
DR   WPI; 2002-090516/12.
DR   P-PSDB; ABB84844.
XX
PT   One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT   useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT   infarction), endothelial or angiogenic disorders in a mammal -
XX
PS   Claim 2; Fig 55; 565pp; English.
XX
CC   ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC   ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
CC   antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
CC   activities, and can be used in gene therapy. The PRO polynucleotides,
CC   proteins, agonists and antagonists are useful for treating or diagnosing
CC   a cardiovascular, endothelial or angiogenic disorder in a mammal,
CC   e.g. cardiac hypertrophy, trauma, cancer, age-related macular
CC   degeneration, atherosclerosis, hypertension, arterial restenosis,
CC   rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
CC   lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
CC   carcinoma) and wound healing. The PRO polynucleotides have applications
CC   in molecular biology, including use as hybridisation probes, and in
CC   chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
CC   probes used in the exemplification of the present invention.
XX
SQ   Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

  Query Match           100.0%;  Score 1679;  DB 24;  Length 1679;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1679;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60

Qy         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120

Qy        121 AAGAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180

Qy        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240

Qy        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300

Qy        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
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Qy       361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420

Qy       421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480

Qy       481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540

Qy       541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600

Qy       601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660

Qy       661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720

Qy       721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAA 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAA 780

Qy       781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840

Qy       841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900

Qy       901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960

Qy       961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020

Qy      1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080

Qy      1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140

Qy      1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200

Qy      1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260

Qy      1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320

Qy      1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380

Qy      1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440
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Qy      1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500

Qy      1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560

Qy      1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620

Qy      1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
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RESULT 7
ABK33598
ID   ABK33598 standard; cDNA; 1679 BP.
XX
AC   ABK33598;
XX
DT   08-MAY-2002  (first entry)
XX
DE   cDNA encoding human PRO protein, Seq ID No 125.
XX
KW   Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW   breast cancer; prostate tumour; rectal tumour; liver tumour;
KW   pericyte cell proliferation; chondrocyte cell proliferation;
KW   tumour necrosis factor-alpha; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200208288-A2.
XX
PD   31-JAN-2002.
XX
PF   29-JUN-2001; 2001WO-US21066.
XX
PR   20-JUL-2000; 2000US-219556P.
PR   25-JUL-2000; 2000US-220585P.
PR   25-JUL-2000; 2000US-220605P.
PR   25-JUL-2000; 2000US-220607P.
PR   25-JUL-2000; 2000US-220624P.
PR   25-JUL-2000; 2000US-220638P.
PR   25-JUL-2000; 2000US-220664P.
PR   25-JUL-2000; 2000US-220666P.
PR   26-JUL-2000; 2000US-220893P.
PR   28-JUL-2000; 2000WO-US20710.
PR   23-AUG-2000; 2000WO-US23522.
PR   24-AUG-2000; 2000WO-US23328.
PR   15-SEP-2000; 2000US-000000P.
PR   10-NOV-2000; 2000WO-US30873.
PR   28-NOV-2000; 2000US-253646P.
PR   01-DEC-2000; 2000WO-US32678.
PR   20-DEC-2000; 2000US-0747259.
PR   20-DEC-2000; 2000WO-US34956.
PR   28-FEB-2001; 2001WO-US06520.
PR   10-MAY-2001; 2001US-0854280.
PR   25-MAY-2001; 2001WO-US17092.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI   Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
DR   WPI; 2002-172001/22.
DR   P-PSDB; AAU83654.
XX
PT   One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT   useful for treating a PRO related disorder and for diagnosing tumours
PT   such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
```

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PT   tumour or liver tumour -
XX
PS   Claim 2; Figure 125; 359pp; English.
XX
CC   The invention relates to one hundred and twenty two nucleic acids
CC   encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
CC   encode human secreted proteins. The PRO nucleic acids, polypeptides,
CC   agonists and antagonists are useful for treating a PRO related disorder.
CC   The PRO polypeptides are useful for diagnosing tumours, especially lung
CC   cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
CC   liver tumour. The PRO polypeptides are useful for stimulating the
CC   proliferation of, or gene expression, in pericyte cells, for stimulating
CC   the proliferation or differentiation of chondrocyte cells, for
CC   stimulating the release of tumour necrosis factor-alpha from human blood,
CC   for stimulating or inhibiting the proliferation of normal human dermal
CC   fibroblast cells. The PRO polypeptide may also be used as molecular
CC   weight markers and for tissue typing. The PRO nucleic acids have
CC   applications in molecular biology, including use as hybridisation probes,
CC   and in chromosome and gene mapping. ABK33536-ABK33657 represent human
CC   PRO protein coding sequences of the invention.
XX
SQ   Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

  Query Match           100.0%;  Score 1679;  DB 24;  Length 1679;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1679;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60

Qy         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120

Qy        121 AAGAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180

Qy        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240

Qy        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCCACCCTCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCCACCCTCAG 300

Qy        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360

Qy        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420

Qy        421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480

Qy        481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540

Qy        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600

Qy        601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660

Qy        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720

Qy        721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCCGTGGTACGGAGAGTAAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCCGTGGTACGGAGAGTAAA 780

Qy        781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840

Qy        841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900

Qy        901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960

Qy        961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020

Qy       1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080

Qy       1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140

Qy       1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200

Qy       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260

Qy       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320

Qy       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380

Qy       1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440

Qy       1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500

Qy       1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560
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Db       1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560

Qy       1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620

Qy       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679


RESULT 8
ACA60526
ID   ACA60526 standard; cDNA; 1679 BP.
XX
AC   ACA60526;
XX
```

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DT   11-JUN-2003  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
XX
KW   Human; secreted and transmembrane polypeptide; PRO;
KW   fibroblast growth factor receptor; PRO533; PRO301; PRO187; PRO337;
KW   PRO1411; PRO10096; PRO246; PRO6307; PRO6003; FGFR-3; FGFR-4; FGFR-1;
KW   FGFR-2; PRO6004; PRO4356; PRO2630; PRO265; PRO951; bioactive molecule;
KW   toxin; radiolabel; antibody; cell death; chromosome mapping;
KW   gene mapping; transgenic animal; knockout animal; gene therapy;
KW   tissue typing; gene; ss.
XX
OS   Homo sapiens.
XX
PN   US2002177165-A1.
XX
PD   28-NOV-2002.
XX
PF   01-FEB-2002; 2002US-0066500.
XX
PR   14-JUL-1998;   98WO-US14552.
PR   10-SEP-1998;   98WO-US18824.
PR   14-SEP-1998;   98WO-US19093.
PR   16-SEP-1998;   98WO-US19330.
PR   17-SEP-1998;   98WO-US19437.
PR   20-NOV-1998;   98WO-US24855.
PR   25-NOV-1998;   98WO-US25190.
PR   01-DEC-1998;   98WO-US25108.
PR   08-MAR-1999;   99WO-US05028.
PR   02-JUN-1999;   99WO-US12252.
PR   01-SEP-1999;   99WO-US20111.
PR   08-SEP-1999;   99WO-US20594.
PR   15-SEP-1999;   99WO-US21090.
PR   15-SEP-1999;   99WO-US21547.
PR   30-NOV-1999;   99WO-US28313.
PR   01-DEC-1999;   99WO-US28301.
PR   02-DEC-1999;   99WO-US28565.
PR   20-DEC-1999;   99WO-US30999.
PR   05-JAN-2000; 2000WO-US00219.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   22-FEB-2000; 2000WO-US04414.
PR   01-MAR-2000; 2000WO-US05601.
PR   02-MAR-2000; 2000WO-US05841.
PR   09-MAR-2000; 2000WO-US06471.
PR   20-MAR-2000; 2000WO-US07377.
PR   30-MAR-2000; 2000WO-US08439.
PR   15-MAY-2000; 2000WO-US13358.
PR   17-MAY-2000; 2000WO-US13705.
PR   22-MAY-2000; 2000WO-US14042.
PR   30-MAY-2000; 2000WO-US14941.
PR   02-JUN-2000; 2000WO-US15264.
PR   11-AUG-2000; 2000WO-US22031.
PR   23-AUG-2000; 2000WO-US23522.
PR   24-AUG-2000; 2000WO-US23328.
PR   01-DEC-2000; 2000WO-US32678.
PR   28-FEB-2001; 2001WO-US06520.
PR   30-MAY-2001; 2001WO-US17443.
PR   01-JUN-2001; 2001WO-US17800.
PR   20-JUN-2001; 2001WO-US19692.
PR   29-JUN-2001; 2001WO-US21066.
PR   09-JUL-2001; 2001WO-US21735.
PR   26-AUG-1997;   97US-056974P.
PR   17-SEP-1997;   97US-059115P.
PR   18-SEP-1997;   97US-059263P.
PR   19-SEP-1997;   97US-059588P.
PR   17-OCT-1997;   97US-062285P.
PR   24-OCT-1997;   97US-062816P.
PR   24-OCT-1997;   97US-063082P.
PR   27-OCT-1997;   97US-063329P.
PR   29-OCT-1997;   97US-063733P.
PR   21-NOV-1997;   97US-066364P.
PR   25-NOV-1997;   97US-066840P.
PR   16-DEC-1997;   97US-069694P.
PR   09-FEB-1998;   98US-074086P.
PR   09-FEB-1998;   98US-074092P.
PR   25-MAR-1998;   98US-079294P.
PR   08-APR-1998;   98US-081049P.
PR   10-AUG-1998;   98US-095998P.
PR   18-AUG-1998;   98US-097000P.
PR   09-SEP-1998;   98US-099601P.
PR   10-SEP-1998;   98US-099803P.
PR   10-SEP-1998;   98US-099811P.
PR   10-SEP-1998;   98US-099812P.
PR   17-SEP-1998;   98US-100858P.
PR   24-SEP-1998;   98US-101922P.
PR   28-OCT-1998;   98US-106032P.
PR   20-NOV-1998;   98US-109304P.
PR   23-MAR-1999;   99US-125778P.
PR   15-JUN-1999;   99US-139695P.
PR   20-JUL-1999;   99US-145070P.
PR   26-JUL-1999;   99US-145698P.
PR   17-AUG-1999;   99US-149396P.
PR   07-DEC-1999;   99US-169495P.
PR   15-NOV-2001; 2001US-0002796.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Botstein DA,  Desnoyers L,  Eaton DL;
PI   Ferrara N,  Fong S,  Gao W,  Gerber H,  Gerritsen ME,  Goddard A;
PI   Godowski PJ,  Gurney AL,  Kljavin IJ,  Mather JP,  Napier MA,  Pan J;
PI   Paoni NF,  Roy MA,  Stewart TA,  Tumas D,  Watanabe CK,  Williams PM;
PI   Wood WI,  Zhang Z;
XX
DR   WPI; 2003-328482/31.
DR   P-PSDB; ABU72061.
XX
PT   Novel secreted and transmembrane polypeptide for modulating biological
PT   activity of cell expressing the polypeptide, for identifying agonists
PT   or antagonists of polypeptide, and as molecular weight markers -
XX
PS   Claim 2; Fig 51; 254pp; English.
XX
CC   The invention describes an isolated, secreted and transmembrane
CC   polypeptide (PP), termed PRO PP or fibroblast growth factor receptor PP
CC   (I). (I) is useful for detecting PRO533, PRO301, PRO187, PRO337,
CC   PRO1411, PRO10096, PRO246, PRO6307, PRO6003, fibroblast growth factor
CC   receptor (FGFR)-3, FGFR-4, FGFR-1, FGFR-2, PRO6004, PRO4356, PRO2630,
CC   PRO265 or PRO951 polypeptide, and for linking a bioactive molecule to a
CC   cell expressing the above polypeptides. The bioactive molecule, a toxin,
CC   radiolabel or an antibody, causes cell death. PRO is useful in assays to
CC   identify other proteins or molecules involved in binding interaction.
CC   The polynucleotide (II) encoding (I) is useful in chromosome and gene
CC   mapping, in generation of antisense RNA and DNA, for generating
CC   transgenic animals or knockout animals which in turn are useful in the
CC   development and screening of therapeutically useful reagents, to
CC   construct hybridisation probes for mapping the gene which encodes the
CC   PRO and for the genetic analysis of individuals with genetic disorders,
CC   in gene therapy, for chromosome identification and as a chromosome
CC   marker. (I) and (II) are useful for tissue typing. This sequence
CC   encodes a novel human secreted and transmembrane PRO polypeptide.
XX
SQ   Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

  Query Match          100.0%;  Score 1679;  DB 25;  Length 1679;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1679;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60
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Db        1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60

Qy       61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120
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Qy      121 AAGAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180
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Db      121 AAGAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180

Qy      181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240

Qy      241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300

Qy      301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360

Qy      361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420

Qy      421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480

Qy      481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540

Qy      541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600

Qy      601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660

Qy      661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720

Qy      721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAA 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAA 780

Qy      781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840

Qy      841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900

Qy      901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960

Qy      961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020

Qy     1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080

Qy     1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140

Qy     1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200

Qy     1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260

Qy     1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320

Qy     1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380

Qy     1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440

Qy     1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500
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Db     1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500

Qy     1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560

Qy     1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620

Qy     1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
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Db     1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
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RESULT 9
ACA03790
ID ACA03790 standard; cDNA; 1679 BP.
XX
AC ACA03790;
XX
DT 23-MAY-2003 (first entry)
XX
DE cDNA encoding human PRO polypeptide #188.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
KW differentiation; chondrocyte; tumour; genetic disorder;
KW cytostatic; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003036180-A1.
XX
PD 20-FEB-2003.
XX
PF 09-MAY-2002; 2002US-0143114.
XX
PR 31-MAR-1997; 97WO-US05230.
PR 12-JUN-1998; 98WO-US12456.
PR 14-JUL-1998; 98WO-US14552.
PR 28-AUG-1998; 98WO-US17888.
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19093.
PR 14-SEP-1998; 98WO-US19094.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 29-OCT-1998; 98WO-US22991.
PR 29-OCT-1998; 98WO-US22992.
PR 20-NOV-1998; 98WO-US24855.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US05190.

PR 20-APR-1999; 99WO-US08615.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 22-DEC-1999; 99WO-US30720.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05746.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 20-DEC-2000; 2000US-0747259.
PR 28-FEB-2001; 2001US-0796498.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 18-MAY-2001; 2001US-0860216.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 21-JUN-2001; 2001US-0887879.
PR 18-JUL-2001; 2001US-0908827.
PR 06-AUG-2001; 2001US-0924419.
PR 09-AUG-2001; 2001US-0927796.
PR 16-AUG-2001; 2001US-0931836.
PR 19-DEC-2001; 2001US-0028072.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-332040/31.
DR P-PSDB; ABU66757.
XX
PT New secreted and transmembrane PRO nucleic acids, useful for gene
PT therapy, in chromosome and gene mapping, as chromosome markers, in
PT tissue typing, and in chromosome identification -
XX
PS Claim 2; Fig 375; 660pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The
CC PRO polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for
CC linking bioactive molecules to cells expressing PRO polypeptides,
CC for modulating biological activities of cells expressing PRO
CC polypeptides, and for for identifying agonists or antagonists.
CC The PRO polypeptides are useful for for stimulating the release of
CC tumour necrosis factor (TNF)-alpha from human blood, for stimulating
CC the proliferation or differentiation of chondrocytes, and detecting the
CC presence of tumours. The polynucleotide sequences encoding PRO
CC polypeptides are useful as hybridisation probes, in chromosome and
CC gene mapping, in the generation of antisense RNA and DNA, in the
CC preparation of PRO polypeptides, for generating transgenic animals or
CC knockout animals, for the genetic analysis of individuals with genetic
CC disorders, and in gene therapy. ACA03603-ACA03877 represent cDNAs
CC encoding the human PRO polypeptides of the invention.
CC Note: The sequence data for this patent was obtained in electronic
CC format directly from the USPTO web site at
CC seqdata.uspto.gov/psipsDIDEntry.html.
XX
SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

Query Match 100.0%; Score 1679; DB 25; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60
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Db          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60

Qy         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 AAGAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180
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Db        121 AAGAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180

Qy        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240
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Db        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240

Qy        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300
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Db        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300

Qy        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
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Db        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360

Qy        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420
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Db        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420

Qy        421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
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Db        421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480

Qy        481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540
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Db        481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540

Qy        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
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Db        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600

Qy        601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660
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Db        601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660

Qy        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
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Db        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720

Qy        721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAA 780
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Db        721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAA 780

Qy        781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840
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Db        781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840

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Db        841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900

Qy        901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960
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Db        901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960

Qy        961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020
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Db        961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020

Qy       1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080
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Db       1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080

Qy       1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140
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Qy       1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200
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Qy       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320
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Db       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320

Qy       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380
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Db       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380

Qy       1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440
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Qy       1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500
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Db       1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500

Qy       1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560
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Qy       1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620
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RESULT 10
ACA04211
ID ACA04211 standard; cDNA; 1679 BP.
XX
AC ACA04211;
XX
DT 27-MAY-2003 (first entry)
XX
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 375.
XX
KW Human; ss; gene; secreted protein; transmembrane protein; PRO;
KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
KW infertility; birth defects; premature aging; AIDS; biosensor;
KW acquired immunodeficiency syndrome; cancer; diabetic complication;
KW bioreactor; tumour.
XX
OS Homo sapiens.
XX
PN US2003032155-A1.
XX
PD 13-FEB-2003.
XX
PF 03-MAY-2002; 2002US-0137865.
XX
PR 31-MAR-1997; 97WO-US05230.
PR 12-JUN-1998; 98WO-US12456.
PR 14-JUL-1998; 98WO-US14552.
PR 28-AUG-1998; 98WO-US17888.
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19093.
PR 14-SEP-1998; 98WO-US19094.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 29-OCT-1998; 98WO-US22991.
PR 29-OCT-1998; 98WO-US22992.
PR 20-NOV-1998; 98WO-US24855.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US05190.
PR 20-APR-1999; 99WO-US08615.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28301.

PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
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PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 22-DEC-1999; 99WO-US30720.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05746.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 20-DEC-2000; 2000US-0747259.
PR 28-FEB-2001; 2001US-0796498.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 18-MAY-2001; 2001US-0860216.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 21-JUN-2001; 2001US-0887879.
PR 18-JUL-2001; 2001US-0908827.
PR 06-AUG-2001; 2001US-0924419.
PR 09-AUG-2001; 2001US-0927796.
PR 16-AUG-2001; 2001US-0931836.
PR 19-DEC-2001; 2001US-0028072.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-331925/31.
DR P-PSDB; ABU67033.
XX
PT New secreted and transmembrane nucleic acids and polypeptides,
PT designated as PRO, useful for treating inflammation, organ failure,
PT atherosclerosis, cardiac injury, infertility, birth defects, premature
PT aging, AIDS, or cancer
XX
PS Claim 2; Fig 375; 659pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising, or which is
CC at least 80% identical to, or the full-length coding sequence of, any of
CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
CC (one of 275 secreted or transmembrane proteins). The nucleic acid
CC further comprises the full-length coding sequence of the DNA deposited
CC under American Type Culture Collection (ATCC) accession number in a list
CC given in the specification. Also included are vectors and host
CC cells for producing PRO proteins, PRO fusion proteins, anti-PRO
CC antibodies, PRO extracellular domains and mature sequences, methods
CC of detecting PRO proteins, methods for stimulating the release of
CC TNF-alpha (tumour necrosis factor alpha) from human blood,
CC (and the proliferation of differentiation of chondrocyte cells, the
CC proliferation of, or gene expression in pericyte cells, the release or
CC proteoglycans from cartilage, proliferation of inner ear urticular
CC supporting cells, the proliferation of T-lymphocyte cells, the release
CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the
CC proliferation of endothelial cells), a method for modulating the uptake
CC of glucose or free fatty acid (FFA) by skeletal muscle cells,
CC a method for inhibiting the binding of A-peptide to factor VIIA,
CC or the differentiation of adipocyte cells, a method for detecting the
CC presence of a tumour in a mammal and an oligonucleotide probe derived
CC from any of the nucleotide sequences cited above. The nucleic acids and
CC polypeptides are useful for treating inflammatory diseases, organ
CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or
CC diabetic complications. The nucleic acids are useful as hybridisation
CC probes, in chromosome and gene mapping, and in generating antisense RNA
CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
CC biosensors or bioreactors. Both are useful in tissue typing.
CC The present sequence encodes a PRO protein of the invention.
XX
SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

Query Match 100.0%; Score 1679; DB 25; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60

Qy         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120

Qy        121 AAGAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180

Qy        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240

Qy        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300

Qy        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
```

```
Qy       361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420

Qy       421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480

Qy       481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540

Qy       541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
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Db       541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600

Qy       601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660

Qy       661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720

Qy       721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAA 780
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Db       721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAA 780

Qy       781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840
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Db       781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840

Qy       841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900

Qy       901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960
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Db       901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960

Qy       961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020
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Db       961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020

Qy      1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080

Qy      1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140

Qy      1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200

Qy      1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
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Db      1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260

Qy      1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320
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Db      1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320

Qy      1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380
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Db      1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380

Qy      1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440
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Db      1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440

Qy      1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500
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Db      1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500

Qy      1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560
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Db      1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560

Qy      1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620
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Db      1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620

Qy      1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
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Db      1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
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RESULT 11
ACA04516
ID ACA04516 standard; cDNA; 1679 BP.
XX
AC ACA04516;
XX
DT 28-MAY-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO337 DNA.
XX
KW Secreted and transmembrane polypeptide; PRO polypeptide; PRO533;
KW PRO301; PRO187; PRO337; PRO1411; PRO10096; PRO246; PRO6307; PRO6003;
KW PRO6004; PRO4356; PRO2630; PRO265; PRO941; FGFR; bioactive molecule;
KW fibroblast growth factor receptor; cell death; chromosome mapping;
KW gene mapping; transgenic animal; knockout animal; gene therapy;
KW tumour; obesity; diabetes; insulinaemia; vascular permeability;
KW cardiac insufficiency disorder; immune response; hearing loss;
KW auditory hair cell regeneration; bone disorder; cartilage disorder;
KW sports injury; arthritis; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003032062-A1.
XX
PD 13-FEB-2003.
XX
PF 01-FEB-2002; 2002US-0066273.
XX
PR 14-JUL-1998; 98WO-US14552.
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19093.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 20-NOV-1998; 98WO-US24855.
PR 25-NOV-1998; 98WO-US25190.
PR 01-DEC-1998; 98WO-US25108.
PR 08-MAR-1999; 99WO-US05028.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28565.
PR 20-DEC-1999; 99WO-US30999.
PR 05-JAN-2000; 2000WO-US00219.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 09-MAR-2000; 2000WO-US06471.
PR 20-MAR-2000; 2000WO-US07377.
PR 30-MAR-2000; 2000WO-US08439.
PR 15-MAY-2000; 2000WO-US13358.
PR 17-MAY-2000; 2000WO-US13705.

PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 01-DEC-2000; 2000WO-US32678.
PR 28-FEB-2001; 2001WO-US06520.
PR 30-MAY-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 26-AUG-1997; 97US-056974P.
PR 17-SEP-1997; 97US-059115P.
PR 18-SEP-1997; 97US-059263P.
PR 19-SEP-1997; 97US-059588P.
PR 17-OCT-1997; 97US-062285P.
PR 24-OCT-1997; 97US-062816P.
PR 24-OCT-1997; 97US-063082P.
PR 27-OCT-1997; 97US-063329P.
PR 29-OCT-1997; 97US-063733P.
PR 21-NOV-1997; 97US-066364P.
PR 25-NOV-1997; 97US-066840P.
PR 16-DEC-1997; 97US-069694P.
PR 09-FEB-1998; 98US-074086P.
PR 09-FEB-1998; 98US-074092P.
PR 25-MAR-1998; 98US-079294P.
PR 08-APR-1998; 98US-081049P.
PR 10-AUG-1998; 98US-095998P.
PR 18-AUG-1998; 98US-097000P.
PR 09-SEP-1998; 98US-099601P.
PR 10-SEP-1998; 98US-099803P.
PR 10-SEP-1998; 98US-099811P.
PR 10-SEP-1998; 98US-099812P.
PR 17-SEP-1998; 98US-100858P.
PR 24-SEP-1998; 98US-101922P.
PR 28-OCT-1998; 98US-106032P.
PR 20-NOV-1998; 98US-109304P.
PR 23-MAR-1999; 99US-125778P.
PR 15-JUN-1999; 99US-139695P.
PR 20-JUL-1999; 99US-145070P.
PR 26-JUL-1999; 99US-145698P.
PR 17-AUG-1999; 99US-149396P.
PR 07-DEC-1999; 99US-169495P.
PR 15-NOV-2001; 2001US-0002796.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;
XX
DR WPI; 2003-341963/32.
DR P-PSDB; ABU67162.
XX
PT New secreted and transmembrane polypeptide for modulating biological
PT activity of a cell expressing the polypeptide, identifying agonists or
PT antagonists of the polypeptide, and as molecular weight markers -
XX
PS Claim 2; Fig 51; 254pp; English.
XX
CC The invention describes an isolated, secreted and transmembrane
CC polypeptide (I), termed PRO polypeptide. (I) Is useful for detecting
CC PRO533, PRO301, PRO187, PRO337, PRO1411, PRO10096, PRO246, PRO6307,
CC PRO6003, PRO6004, PRO4356, PRO2630, PRO265, PRO941, fibroblast growth
CC factor receptor (FGFR)-4, FGFR-3, FGFR-2 or FGFR-1 polypeptide, and for
CC linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a
CC cell expressing the polypeptides. The bioactive molecule causes cell
CC death. (II) Is useful as hybridisation probes, in chromosome and gene
CC mapping, in generation of antisense RNA and DNA, in the preparation of
CC PRO polypeptide, for generating transgenic animals or knockout animals
CC which in turn are useful in the development and screening of
CC therapeutically useful reagents, and for the genetic analysis of
CC individuals with genetic disorders, in gene therapy, and for chromosome
CC identification. (I) Or Ab is useful for the preparation of medicament for
CC treating conditions which are responsive to the PRO polypeptide or
CC anti-PRO antibody e.g. a tumour. (I) is useful for treating obesity,
CC diabetes or hypo- or hyper-insulinaemia, and cardiac insufficiency
CC disorders, for inhibiting tumour growth, enhances vascular permeability
CC and immune response, for inducing regeneration of auditory hair cells and
CC for treating hearing loss in mammals, and for treating bone and/or
CC cartilage disorders such as sports injuries and arthritis. This sequence
CC encodes a novel human secreted and transmembrane polypeptide.
XX
SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

Query Match 100.0%; Score 1679; DB 25; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60

Qy         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120

Qy        121 AAGAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180

Qy        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240
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Db        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240

Qy        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300
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Db        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300

Qy        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360

Qy        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420
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Db        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420

Qy        421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
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Qy        481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540
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Db        481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540

Qy        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600

Qy        601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660

Qy        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
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Db        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720

Qy        721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCCGTGGTACGGAGAGTAAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCCGTGGTACGGAGAGTAAA 780

Qy        781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840
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Db        781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840

Qy        841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900
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Db        841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900

Qy        901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960
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Db        901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960

Qy        961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020
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Db        961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020

Qy       1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080

Qy       1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140
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Qy       1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200
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Db       1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200

Qy       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
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Db       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260

Qy       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320
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Qy       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380
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Db       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380

Qy       1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440

Qy       1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500

Qy       1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560

Qy       1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620

Qy       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679


RESULT 12
ACA04996
ID   ACA04996 standard; cDNA; 1679 BP.
XX
AC   ACA04996;
XX
DT   28-MAY-2003 (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
XX
KW   Secreted and transmembrane polypeptide; PRO polypeptide; PRO533;
KW   PRO301; PRO187; PRO337; PRO1411; PRO10096; PRO246; PRO6307; PRO6003;
KW   PRO6004; PRO4356; PRO2630; PRO265; PRO941; FGFR; bioactive molecule;
KW   fibroblast growth factor receptor; cell death; chromosome mapping;
KW   gene mapping; transgenic animal; knockout animal; gene therapy;
KW   tumour; obesity; diabetes; insulinaemia; vascular permeability;
KW   cardiac insufficiency disorder; immune response; hearing loss;
KW   auditory hair cell regeneration; bone disorder; cartilage disorder;
KW   sports injury; arthritis; gene; ss.
XX
OS   Homo sapiens.
XX
PN   US2003032063-A1.
XX
PD   13-FEB-2003.
XX
PF   01-FEB-2002; 2002US-0066494.
XX
PR   14-SEP-1998;   98WO-US19093.
PR   16-SEP-1998;   98WO-US19330.
PR   17-SEP-1998;   98WO-US19437.
PR   20-NOV-1998;   98WO-US24855.
PR   25-NOV-1998;   98WO-US25190.
PR   01-DEC-1998;   98WO-US25108.
PR   08-MAR-1999;   99WO-US05028.
PR   02-JUN-1999;   99WO-US12252.
PR   01-SEP-1999;   99WO-US20111.
PR   08-SEP-1999;   99WO-US20594.
PR   15-SEP-1999;   99WO-US21090.
PR   15-SEP-1999;   99WO-US21547.
PR   30-NOV-1999;   99WO-US28313.
PR   01-DEC-1999;   99WO-US28301.
PR   02-DEC-1999;   99WO-US28565.
PR   20-DEC-1999;   99WO-US30999.
PR   05-JAN-2000; 2000WO-US00219.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   22-FEB-2000; 2000WO-US04414.
PR   01-MAR-2000; 2000WO-US05601.
PR   02-MAR-2000; 2000WO-US05841.
PR   09-MAR-2000; 2000WO-US06471.
PR   20-MAR-2000; 2000WO-US07377.
PR   30-MAR-2000; 2000WO-US08439.
PR   15-MAY-2000; 2000WO-US13358.
PR   17-MAY-2000; 2000WO-US13705.
PR   22-MAY-2000; 2000WO-US14042.
PR   30-MAY-2000; 2000WO-US14941.
PR   02-JUN-2000; 2000WO-US15264.
PR   11-AUG-2000; 2000WO-US22031.
PR   23-AUG-2000; 2000WO-US23522.
PR   24-AUG-2000; 2000WO-US23328.
PR   01-DEC-2000; 2000WO-US32678.
PR   28-FEB-2001; 2001WO-US06520.
PR   30-MAY-2001; 2001WO-US17443.
PR   01-JUN-2001; 2001WO-US17800.
PR   20-JUN-2001; 2001WO-US19692.
PR   29-JUN-2001; 2001WO-US21066.
PR   09-JUL-2001; 2001WO-US21735.
PR   26-AUG-1997;   97US-056974P.
PR   17-SEP-1997;   97US-059115P.
PR   18-SEP-1997;   97US-059263P.
PR   19-SEP-1997;   97US-059588P.
PR   17-OCT-1997;   97US-062285P.
PR   24-OCT-1997;   97US-062816P.
PR   24-OCT-1997;   97US-063082P.
PR   27-OCT-1997;   97US-063329P.
PR   29-OCT-1997;   97US-063733P.
PR   21-NOV-1997;   97US-066364P.
PR   25-NOV-1997;   97US-066840P.
PR   16-DEC-1997;   97US-069694P.
PR   09-FEB-1998;   98US-074086P.
PR   09-FEB-1998;   98US-074092P.
PR   25-MAR-1998;   98US-079294P.
PR   08-APR-1998;   98US-081049P.
PR   10-AUG-1998;   98US-095998P.
PR   18-AUG-1998;   98US-097000P.
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PR   09-SEP-1998;   98US-099601P.
PR   10-SEP-1998;   98US-099803P.
PR   10-SEP-1998;   98US-099811P.
PR   10-SEP-1998;   98US-099812P.
PR   17-SEP-1998;   98US-100858P.
PR   24-SEP-1998;   98US-101922P.
PR   28-OCT-1998;   98US-106032P.
PR   20-NOV-1998;   98US-109304P.
PR   23-MAR-1999;   99US-125778P.
PR   15-JUN-1999;   99US-139695P.
PR   20-JUL-1999;   99US-145070P.
PR   26-JUL-1999;   99US-145698P.
PR   17-AUG-1999;   99US-149396P.
PR   07-DEC-1999;   99US-169495P.
PR   15-NOV-2001; 2001US-0002796.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Botstein DA,  Desnoyers L,  Eaton DL;
PI   Ferrara N,  Fong S,  Gao W,  Gerber H,  Gerritsen ME,  Goddard A;
PI   Godowski PJ,  Gurney AL,  Kljavin IJ,  Mather JP,  Napier MA,  Pan J;
PI   Paoni NF,  Roy MA,  Stewart TA,  Tumas D,  Watanabe CK,  Williams PM;
PI   Wood WI,  Zhang Z;
XX
DR   WPI; 2003-341964/32.
DR   P-PSDB; ABU67293.
XX
PT   Thirty seven nucleic acids encoding novel secreted and transmembrane
PT   PRO polypeptides, useful for modulating biological activity of cell
PT   expressing the polypeptide, and in chromosome and gene mapping -
XX
PS   Claim 2; Fig 51; 255pp; English.
XX
CC   The invention describes an isolated, secreted and transmembrane
CC   polypeptide (I), termed PRO polypeptide. (I) Is useful for detecting
CC   PRO533, PRO301, PRO187, PRO337, PRO1411, PRO10096, PRO246, PRO6307,
CC   PRO6003, PRO6004, PRO4356, PRO2630, PRO265, PRO941, fibroblast growth
CC   factor receptor (FGFR)-4, FGFR-3, FGFR-2 or FGFR-1 polypeptide, and for
CC   linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a
CC   cell expressing the polypeptides. The bioactive molecule causes cell
CC   death. (II) Is useful as hybridisation probes, in chromosome and gene
CC   mapping, in generation of antisense RNA and DNA, in the preparation of
CC   PRO polypeptide, for generating transgenic animals or knockout animals
CC   which in turn are useful in the development and screening of
CC   therapeutically useful reagents, and for the genetic analysis of
CC   individuals with genetic disorders, in gene therapy, and for chromosome
CC   identification. (I) Or Ab is useful for the preparation of medicament for
CC   treating conditions which are responsive to the PRO polypeptide or
CC   anti-PRO antibody e.g. a tumour. (I) is useful for treating obesity,
CC   diabetes or hypo- or hyper-insulinaemia, and cardiac insufficiency
CC   disorders, for inhibiting tumour growth, enhances vascular permeability
CC   and immune response, for inducing regeneration of auditory hair cells and
CC   for treating hearing loss in mammals, and for treating bone and/or
CC   cartilage disorders such as sports injuries and arthritis. This sequence
CC   encodes a novel human secreted and transmembrane polypeptide
CC   associated oligonucleotide.
XX
SQ   Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

  Query Match           100.0%;  Score 1679;  DB 25;  Length 1679;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1679;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60

Qy         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120

Qy        121 AAGAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        121 AAGAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180

Qy        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240

Qy        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300

Qy        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360

Qy        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420

Qy        421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480

Qy        481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540

Qy        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600

Qy        601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660

Qy        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720

Qy        721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAA 780

Qy        781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840

Qy        841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900

Qy        901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960

Qy        961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020

Qy       1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080

Qy       1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140

Qy       1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200

Qy       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
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Qy       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320
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Db       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320

Qy       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380
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Db       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380

Qy       1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440

Qy       1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500

Qy       1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560

Qy       1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620

Qy       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
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RESULT 13
ABX89328
ID ABX89328 standard; cDNA; 1679 BP.
XX
AC ABX89328;
XX
DT 13-MAY-2003 (first entry)
XX
DE DNA encoding novel secreted and transmembrane protein PRO337.
XX
KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosum; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpetiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003017563-A1.
XX
PD 23-JAN-2003.
XX
PF 07-MAY-2002; 2002US-0140808.
XX
PR 31-MAR-1997; 97WO-US05230.
PR 12-JUN-1998; 98WO-US12456.
PR 14-JUL-1998; 98WO-US14552.
PR 28-AUG-1998; 98WO-US17888.
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19093.
PR 14-SEP-1998; 98WO-US19094.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 29-OCT-1998; 98WO-US22991.
PR 29-OCT-1998; 98WO-US22992.
PR 20-NOV-1998; 98WO-US24855.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US05190.
PR 20-APR-1999; 99WO-US08615.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 22-DEC-1999; 99WO-US30720.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05746.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 20-DEC-2000; 2000US-0747259.
PR 28-FEB-2001; 2001US-0796498.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 18-MAY-2001; 2001US-0860216.

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PR   25-MAY-2001; 2001US-0866028.
PR   25-MAY-2001; 2001US-0866034.
PR   01-JUN-2001; 2001US-0872035.
PR   05-JUN-2001; 2001US-0874503.
PR   14-JUN-2001; 2001US-0882636.
PR   19-JUN-2001; 2001US-0886342.
PR   21-JUN-2001; 2001US-0887879.
PR   18-JUL-2001; 2001US-0908827.
PR   06-AUG-2001; 2001US-0924419.
PR   09-AUG-2001; 2001US-0927796.
PR   16-AUG-2001; 2001US-0931836.
PR   19-DEC-2001; 2001US-0028072.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI   Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI   Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR   WPI; 2003-148238/14.
DR   P-PSDB; ABU59838.
XX
PT   Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT   and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT   are therapeutically useful for enhancing immune response and in cancer
PT   treatments
XX
PS   Claim 2; Fig 375; 659pp; English.
XX
CC   The invention describes an isolated human PRO polypeptide. The PRO
CC   polypeptides are useful in detecting PRO polypeptides in a sample, in
CC   linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC   in modulating at least one biological activity of a cell expressing a PRO
CC   polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC   useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC   stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC   PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC   PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC   useful for treating conditions or disorders where angiogenesis would be
CC   beneficial, e.g. wound healing and antagonist of this polypeptide are
CC   useful for treating cancerous tumours. PRO812 inhibits vascular
CC   endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC   cells and is thus useful for inhibiting endothelial cell growth in
CC   mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC   PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC   stimulated T-lymphocytes and are therapeutically useful for enhancing
CC   immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC   retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC   rod photoreceptor cells) and therefore are useful for treating retinal
CC   disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813
CC   and PRO11066 induce proliferation of mammalian kidney mesangial cells,
CC   and therefore are useful for treating kidney disorders associated with
CC   decreased mesangial cell function such as Berger disease or other
CC   nephropathies associated with dermatitis, herpetiformis or Crohn's
CC   disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC   proliferation and/or redifferentiation of chondrocytes in culture and
CC   are thus useful for treating sports injuries, and arthritis. This
CC   sequence encodes a novel human PRO protein.
XX
SQ   Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

  Query Match           100.0%;  Score 1679;  DB 25;  Length 1679;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1679;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60

Qy         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120

Qy        121 AAGAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180

Qy        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240

Qy        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300

Qy        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360

Qy        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420

Qy        421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
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Db        421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480

Qy        481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540
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Db        481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540

Qy        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600

Qy        601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660

Qy        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
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Db        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720

Qy        721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCCGTGGTACGGAGAGTAAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCCGTGGTACGGAGAGTAAA 780

Qy        781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840
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Db        781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840

Qy        841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900

Qy        901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960
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Db        901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960

Qy        961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020

Qy       1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080

Qy       1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140

Qy       1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200

Qy       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
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Db       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260

Qy       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320

Qy       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380
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Db       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380

Qy       1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440
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Qy       1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500
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Db       1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500

Qy       1501 TCTGCCCACAGAGTGCCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560
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Db       1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560

Qy       1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620
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Db       1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620

Qy       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
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Db       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
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RESULT 14
ABX92696
ID ABX92696 standard; cDNA; 1679 BP.
XX
AC ABX92696;
XX
DT 08-MAY-2003 (first entry)
XX
DE cDNA encoding human PRO337 polypeptide.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;
KW cardiac insufficiency; nervous system disorder; kidney disorder;
KW bone disorder; cartilage disorder; arthritis; tumour; wound healing;
KW genetic disorder; cytostatic; antidiabetic; antiinflammatory;
KW antiarthritic; anti-tumour; vulnerary; antianaemic; dermatological;
KW cardiant; gene; ss.
XX
OS Homo sapiens.
XX
PN US2002169284-A1.
XX
PD 14-NOV-2002.
XX
PF 16-OCT-2001; 2001US-0978697.
XX
PR 07-OCT-1998; 98WO-US21141.
PR 20-NOV-1998; 98WO-US24855.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US05190.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 30-NOV-1999; 99WO-US28313.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 24-FEB-2000; 2000WO-US05004.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 24-AUG-2000; 2000WO-US23328.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 22-MAR-2001; 2001WO-US09552.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 17-OCT-1997; 97US-062250P.
PR 03-NOV-1997; 97US-064249P.
PR 13-NOV-1997; 97US-065311P.
PR 21-NOV-1997; 97US-066364P.
PR 10-MAR-1998; 98US-077450P.
PR 11-MAR-1998; 98US-077632P.
PR 11-MAR-1998; 98US-077641P.
PR 11-MAR-1998; 98US-077649P.
PR 12-MAR-1998; 98US-077791P.
PR 13-MAR-1998; 98US-078004P.
PR 20-MAR-1998; 98US-078886P.
PR 20-MAR-1998; 98US-078910P.
PR 20-MAR-1998; 98US-078936P.
PR 20-MAR-1998; 98US-078939P.
PR 25-MAR-1998; 98US-079294P.
PR 26-MAR-1998; 98US-079656P.
PR 27-MAR-1998; 98US-079663P.
PR 27-MAR-1998; 98US-079664P.
PR 27-MAR-1998; 98US-079689P.
PR 27-MAR-1998; 98US-079728P.
PR 27-MAR-1998; 98US-079786P.
PR 30-MAR-1998; 98US-079920P.
PR 30-MAR-1998; 98US-079923P.
PR 26-MAY-1981; 81US-0267213.
PR 17-MAR-1998; 98US-0040220.
PR 26-JUN-1998; 98US-0105413.
PR 07-OCT-1998; 98US-0168978.
PR 02-NOV-1998; 98US-0184216.
PR 06-NOV-1998; 98US-0187368.
PR 07-DEC-1998; 98US-0202054.
PR 22-DEC-1998; 98US-0218517.
PR 05-MAR-1999; 99US-0254465.
PR 10-MAR-1999; 99US-0265686.
PR 12-APR-1999; 99US-0284291.
PR 14-MAY-1999; 99US-0311832.
PR 14-MAY-1999; 99US-0380137.
PR 25-AUG-1999; 99US-0380138.
PR 25-AUG-1999; 99US-0380142.
PR 08-NOV-2000; 2000US-0709238.
PR 27-NOV-2000; 2000US-0723749.
PR 20-DEC-2000; 2000US-0747259.
PR 22-MAR-2001; 2001US-0816744.
PR 22-MAR-2001; 2001US-0816920.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 30-JUL-2001; 2001US-0918585.

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XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi A,  Baker KP,  Botstein D,  Desnoyers L,  Eaton D;
PI   Ferrara N,  Filvaroff E,  Fong S,  Gao W,  Gerber H,  Gerritsen ME;
PI   Goddard A,  Godowski PJ,  Grimaldi JC,  Gurney AL,  Hillan KJ;
PI   Kljavin IJ,  Kuo SS,  Napier MA,  Pan J,  Paoni NF,  Roy MA;
PI   Shelton DL,  Stewart TA,  Tumas D,  Williams PM,  Wood WI;
XX
DR   WPI; 2003-288163/28.
DR   P-PSDB; ABU61159.
XX
PT   Novel secreted and transmembrane polypeptides and polynucleotides
PT   encoding them useful for treating cancer, kidney diseases, bone,
PT   cartilage disorders and immune deficiencies  -
XX
PS   Claim 2; Fig 221; 459pp; English.
XX
CC   The present invention relates to the isolation of novel human PRO
CC   polypeptides, and the polynucleotide sequences encoding them. The
CC   PRO polypeptides are secreted and transmembrane proteins. The PRO
CC   polypeptides are useful for detecting other PRO polypeptides, for
CC   linking bioactive molecules to cells expressing PRO polypeptides,
CC   for modulating biological activities of cells expressing PRO
CC   polypeptides, and for for identifying agonists or antagonists. The
CC   bioactive molecule maybe a toxin, radiolabel or antibody, and causes
CC   apoptosis or death of the cell. The PRO polypeptides are useful for
CC   treating immune disorders, diabetes or hyper- or hypo-insulinaemia,
CC   cardiac insufficiency, nervous system disorders, kidney disorders,
CC   bone and cartilage disorders or arthritis, tumours, and wound healing.
CC   The polynucleotide sequences encoding PRO polypeptides are useful as
CC   hybridisation probes, in chromosome and gene mapping, in the generation
CC   of antisense RNA and DNA, in the preparation of PRO polypeptides, for
CC   generating transgenic animals or knockout animals, for the genetic
CC   analysis of individuals with genetic disorders, and in gene therapy.
CC   The present sequence encodes a human PRO polypeptide of the invention.
CC   Note: The sequence data for this patent was obtained in electronic
CC   format directly from the USPTO web site at
CC   seqdata.uspto.gov/psipsDIDEntry.html.
XX
SQ   Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

  Query Match           100.0%;  Score 1679;  DB 25;  Length 1679;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1679;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60
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Qy         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120
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Db         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120

Qy        121 AAGAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180
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Db        121 AAGAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180

Qy        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240
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Db        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240

Qy        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300
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Db        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300

Qy        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
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Db        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360

Qy        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420
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Db        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420

Qy        421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480

Qy        481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540
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Db        481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540

Qy        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
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Qy        601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660
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Db        601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660

Qy        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
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Db        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720

Qy        721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCCGTGGTACGGAGAGTAAA 780
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Qy        781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840
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Db        781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840

Qy        841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900
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Db        841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900

Qy        901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960

Qy        961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020
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Qy       1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080
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Db       1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080

Qy       1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140

Qy       1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200

Qy       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
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Db       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260

Qy       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320
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Db       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320

Qy       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380

Qy       1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440

Qy       1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500
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Qy       1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560

Qy       1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620

Qy       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679


RESULT 15
AAZ47893
ID   AAZ47893 standard; cDNA; 1693 BP.
XX
AC   AAZ47893;
XX
DT   10-MAR-2000  (first entry)
XX
DE   Human protein encoding cDNA SEQ ID NO:3.
XX
KW   Human; haematopoietic cell regulation; tissue generation; reparation;
KW   activin; inhibin; taxis; chemotaxis; blood coagulation; thrombus;
KW   receptor; ligand; autoimmune; infection-related immunodeficiency;
KW   inflammatory disorder; neurological disease; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             214..1164
FT                   /*tag= a
XX
PN   WO9958668-A1.
XX
PD   18-NOV-1999.
XX
PF   13-MAY-1999;   99WO-JP02485.
XX
PR   14-MAY-1998;   98JP-0131815.
XX
PA   (ONOY ) ONO PHARM CO LTD.
XX
PI   Fukushima D,  Shibayama S,  Tada H;
XX
DR   WPI; 2000-062298/05.
DR   P-PSDB; AAY57601.
XX
PT   New polypeptides of human origin having cell regulatory, tissue
PT   generation, coagulant and other activities
XX
PS   Claim 5; Page 42-45; 84pp; Japanese.
XX
CC   The present sequence encodes a specifically claimed novel human protein.
CC   The novel human protein can be used in therapeutic drugs for the
CC   prevention and treatment of a broad range of disorders including
CC   autoimmune and infection-related immunodeficiency, inflammatory
CC   disorders, and neurological diseases. The novel protein is expected of
CC   having haematopoietic cell regulatory activity, tissue generation/
CC   reparation activity, activin/inhibin activity, taxis/chemotaxis activity,
CC   blood coagulation and thrombus activity, and receptor/ligand activity.
XX
SQ   Sequence 1693 BP; 518 A; 432 C; 416 G; 327 T; 0 other;

  Query Match           99.0%;  Score 1661.4;  DB 21;  Length 1693;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 1673;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          6 GTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACACAATCT 65
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACACAATCT 60

Qy         66 ATCAGGAAAGAAAGAAAG-AAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAGAAGA 124
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db         61 ATCAGGAAAGAAAGAAAGAAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAGAAGA 120

Qy        125 AAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTC 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTC 180

Qy        185 ACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACC 240

Qy        245 TTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGC 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGC 300

Qy        305 ACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCT 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCT 360

Qy        365 GGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAG 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAG 420

Qy        425 TACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTG 484
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Db        421 TACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTG 480

Qy        485 CAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAA 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAA 540

Qy        545 ATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGC 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGC 600

Qy        605 ATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTT 664
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Db        601 ATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTT 660

Qy        665 GGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGG 724
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Qy        725 GACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTC 784
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Qy        785 ACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAA 844
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAA 840

Qy        845 AAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAG 904
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAG 900

Qy        905 GATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTC 964
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTC 960

Qy        965 TCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCC 1024
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCC 1020

Qy       1025 TCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGC 1084
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Qy       1085 GAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTC 1144
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Db       1141 TTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCTGCCG 1200

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Qy       1265 CAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAACAAAG 1324
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Db       1261 CAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAACAAAG 1320

Qy       1325 AATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATATTTA 1384
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Qy       1385 GGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGACCCA 1444
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1445 CTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTCTCTG 1504
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Qy       1505 CCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCAGTCC 1564
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 CCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCAGTCC 1560

Qy       1565 ATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTGGTAG 1624
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTGGTAG 1620

Qy       1625 ACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
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Db       1621 ACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1675
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Search completed: September 10, 2003, 23:22:31
Job time : 575 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 10, 2003, 23:22:37 ; Search time 154 Seconds
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Title: US-10-017-084A-522
Perfect score: 1679
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Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	343	20.4	1238	2	US-08-414-657D-3	Sequence 3, Appli
2	343	20.4	1238	4	US-09-135-080-3	Sequence 3, Appli
3	340.6	20.3	924	2	US-08-414-657D-7	Sequence 7, Appli
4	340.6	20.3	977	2	US-08-414-657D-1	Sequence 1, Appli
5	340.6	20.3	977	4	US-09-135-080-1	Sequence 1, Appli
6	340.6	20.3	1014	2	US-08-414-657D-5	Sequence 5, Appli
7	340.6	20.3	1014	4	US-09-135-080-7	Sequence 7, Appli
8	338.6	20.2	861	2	US-08-414-657D-9	Sequence 9, Appli
9	338.6	20.2	912	2	US-08-414-657D-6	Sequence 6, Appli
10	337.4	20.1	945	2	US-08-414-657D-8	Sequence 8, Appli
11	333.8	19.9	861	2	US-08-414-657D-10	Sequence 10, Appl
12	303.6	18.1	756	2	US-08-414-657D-17	Sequence 17, Appl
13	298.2	17.8	756	2	US-08-414-657D-18	Sequence 18, Appl
14	100	6.0	219	2	US-08-414-657D-11	Sequence 11, Appl
15	95.2	5.7	219	2	US-08-414-657D-12	Sequence 12, Appl
16	77.8	4.6	177	2	US-08-414-657D-13	Sequence 13, Appl
17	77.8	4.6	177	2	US-08-414-657D-14	Sequence 14, Appl
18	65.6	3.9	198	2	US-08-414-657D-15	Sequence 15, Appl
19	63.4	3.8	198	2	US-08-414-657D-16	Sequence 16, Appl
20	50.2	3.0	240	1	US-08-628-417-6	Sequence 6, Appli
21	49.8	3.0	1048	4	US-09-489-847-38	Sequence 38, Appl
22	48.6	2.9	1813	3	US-09-071-224-3	Sequence 3, Appli
23	48.4	2.9	1117	3	US-09-247-373B-33	Sequence 33, Appl
24	47.8	2.8	441	4	US-09-601-537-10	Sequence 10, Appl
25	47.8	2.8	4121	4	US-09-601-537-9	Sequence 9, Appli
26	47.6	2.8	2447	2	US-09-014-969-14	Sequence 14, Appl
27	47.6	2.8	2674	4	US-09-817-180-1	Sequence 1, Appli
28	47.4	2.8	1696	4	US-09-835-811-1	Sequence 1, Appli
29	46.8	2.8	2608	4	US-09-904-615-16	Sequence 16, Appl
30	46.6	2.8	569	4	US-09-461-325-44	Sequence 44, Appl
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32	46.6	2.8	674	4	US-09-620-405B-465	Sequence 465, App
33	46.6	2.8	674	4	US-09-433-826B-465	Sequence 465, App
34	46.6	2.8	674	4	US-09-604-287A-465	Sequence 465, App
35	46.6	2.8	1411	3	US-08-964-127-5	Sequence 5, Appli
36	46.6	2.8	1411	4	US-09-496-692-5	Sequence 5, Appli
37	46.6	2.8	1411	4	US-10-000-273-5	Sequence 5, Appli
38	46.6	2.8	2846	4	US-09-996-243-230	Sequence 230, App
39	46.6	2.8	3275	4	US-09-370-838-151	Sequence 151, App
40	46.4	2.8	140	1	US-08-628-417-5	Sequence 5, Appli
41	46.4	2.8	578	4	US-09-602-877A-95	Sequence 95, Appl
c 42	46.4	2.8	1020	4	US-09-328-475C-43	Sequence 43, Appl
43	46.4	2.8	2246	4	US-09-363-708-3	Sequence 3, Appli
44	46.4	2.8	2246	4	US-09-083-587-3	Sequence 3, Appli
45	46.4	2.8	2280	3	US-08-813-150-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-414-657D-3
; Sequence 3, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1238 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 56...1069
; OTHER INFORMATION:
US-08-414-657D-3

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Query Match            20.4%;  Score 343;  DB 2;  Length 1238;
Best Local Similarity   62.0%;  Pred. No. 2.6e-80;
Matches  598;  Conservative    0;  Mismatches  355;  Indels   12;  Gaps    3;

Qy        205 TCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAA 264
Db        121 TCTTCCCACAGGACTGCCCGTTCGCAGCGTGGAT------TTTAACCGAGGCACGGACAA 174

Qy        265 CGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCAC 324
Db        175 CATCACCGTGAGGCAGGGGGACACGGCCATCCTCAGGTGTGTGGTAGAAGACAAGAACTC 234

Qy        325 CCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCT 384
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Qy        385 GGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAA 444
Db        295 GGACCCTCGGGTTGAGCTGGAGAAACGCCATGCTCTGGAATACAGCCTCCGAATCCAGAA 354

Qy        445 CGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAA 504
Db        355 GGTGGATGTCTATGATGAAGGATCCTACACATGCTCAGTTCAGACACAGCATGAGCCCAA 414

Qy        505 GACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGA 564
Db        415 GACCTCTCAAGTTTACTTGATTGTACAAGTTCCACCAAAGATCTCCAACATCTCCTCGGA 474

Qy        565 TATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGA 624
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Qy        685 ATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC 744
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Qy        745 CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATA 804
Db        655 CAACGAGGTCTCCTCCGCGGATGTCAAACAAGTCAAGGTCACTGTGAACTATCCACCCAC 714

Qy        805 CATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGA 864
Db        715 CATCACAGAGTCTAAGAGCAATGAAGCCACCACAGGACGACAAGCTTCCCTCAAATGTGA 774

Qy        865 AGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGA 924
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Qy       1165 TTGAT 1169
Db       1069 TTAAT 1073
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RESULT 2
US-09-135-080-3
; Sequence 3, Application US/09135080
; Patent No. 6423827
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat R.
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/135,080
;      FILING DATE:  17-AUG-1998
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/414,657
;      FILING DATE:  31-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-620-3214
;      TELEFAX:  609-620-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1238 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  56...1069
;      OTHER INFORMATION:
US-09-135-080-3

  Query Match            20.4%;  Score 343;  DB 4;  Length 1238;
  Best Local Similarity   62.0%;  Pred. No. 2.6e-80;
  Matches  598;  Conservative    0;  Mismatches  355;  Indels   12;  Gaps    3;

Qy        205 TCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAA 264
Db        121 TCTTCCCACAGGACTGCCCGTTCGCAGCGTGGAT------TTTAACCGAGGCACGGACAA 174

Qy        265 CGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCAC 324
Db        175 CATCACCGTGAGGCAGGGGGACACGGCCATCCTCAGGTGTGTGGTAGAAGACAAGAACTC 234

Qy        325 CCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCT 384
Db        235 GAAAGTGGCCTGGTTGAACCGCTCTGGCATCATCTTCGCTGGACACGACAAGTGGTCTCT 294

Qy        385 GGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAA 444
Db        295 GGACCCTCGGGTTGAGCTGGAGAAACGCCATGCTCTGGAATACAGCCTCCGAATCCAGAA 354

Qy        445 CGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAA 504
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Db        355 GGTGGATGTCTATGATGAAGGATCCTACACATGCTCAGTTCAGACACAGCATGAGCCCAA 414

Qy        505 GACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGA 564

Db        415 GACCTCTCAAGTTTACTTGATTGTACAAGTTCCACCAAAGATCTCCAACATCTCCTCGGA 474

Qy        565 TATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGA 624

Db        475 TGTCACTGTGAATGAGGGCAGCAATGTAACCCTGGTCTGCATGGCCAATGGGCGCCCTGA 534

Qy        625 GCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGA 684

Db        535 ACCTGTTATCACCTGGAGACACCTTACACCACTTGGAAGAGAATTTGAAGGAGAAGAAGA 594

Qy        685 ATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC 744

Db        595 ATATCTGGAGATCCTAGGCATCACCAGGGAACAGTCAGGCAAATATGAGTGCAAGGCTGC 654

Qy        745 CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATA 804

Db        655 CAACGAGGTCTCCTCCGCGGATGTCAAACAAGTCAAGGTCACTGTGAACTATCCACCCAC 714

Qy        805 CATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGA 864

Db        715 CATCACAGAGTCTAAGAGCAATGAAGCCACCACAGGACGACAAGCTTCCCTCAAATGTGA 774

Qy        865 AGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGA 924

Db        775 AGCCTCAGCGGTGCCTGCACCTGACTTTGAGTGGTACCGGGATGACACCAG---GATAAA 831

Qy        925 AGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAA 984

Db        832 CAGTGCAAACGGCCTTGAGATTAAGAGCACTGAGGGCCAGTCCTCCCTGACGGTGACCAA 891

Qy        985 TGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACAC 1044

Db        892 CGTCACTGAGGAACACTACGGCAACTATACCTGTGTGGCTGCCAACAAGCTCGGCGTCAC 951

Qy       1045 CAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTC 1104

Db        952 CAATGCCAGCCTAGTCCTTTTCAGACCCGGGTCGGTGAG---AGGAATCAACGGATCCAT 1008

Qy       1105 GAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATT 1164

Db       1009 CAGTCTGGCCGTACCACTGTGGCTGCTGGCAGCGTCCCTGTTCTGCCTTCTCAGCAAATG 1068

Qy       1165 TTGAT 1169

Db       1069 TTAAT 1073
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RESULT 3
US-08-414-657D-7
; Sequence 7, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  924 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...924
;      OTHER INFORMATION:
US-08-414-657D-7

  Query Match           20.3%;  Score 340.6;  DB 2;  Length 924;
  Best Local Similarity  63.3%;  Pred. No. 9.6e-80;
  Matches  558;  Conservative    0;  Mismatches  314;  Indels    9;  Gaps    2;

Qy        205 TCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAA 264

Db         45 TCTTCCCACAGGACTGCCTGTTCGCAGCGTGGAT------TTTAACCGAGGCACGGACAA 98

Qy        265 CGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCAC 324

Db         99 CATCACCGTGAGGCAGGGGGACACAGCCATCCTCAGGTGCGTTCTAGAAGACAAGAACTC 158

Qy        325 CCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCT 384

Db        159 AAAGGTGGCCTGGTTGAACCGTTCTGGCATCATTTTTGCTGGACATGACAAGTGGTCTCT 218

Qy        385 GGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAA 444

Db        219 GGACCCACGGGTTGAGCTGGAGAAACGCCATTCTCTGGAATACAGCCTCCGAATCCAGAA 278

Qy        445 CGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAA 504

Db        279 GGTGGATGTCTATGATGAGGGTTCCTACACTTGCTCAGTTCAGACACAGCATGAGCCCAA 338

Qy        505 GACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGA 564

Db        339 GACCTCCCAAGTTTACTTGATCGTACAAGTCCCACCAAAGATCTCCAATATCTCCTCGGA 398

Qy        565 TATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGA 624

Db        399 TGTCACTGTGAATGAGGGCAGCAACGTGACTCTGGTCTGCATGGCCAATGGCCGTCCTGA 458

Qy        625 GCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGA 684

Db        459 ACCTGTTATCACCTGGAGACACCTTACACCAACTGGAAGGGAATTTGAAGGAGAAGAAGA 518

Qy        685 ATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC 744

Db        519 ATATCTGGAGATCCTTGGCATCACCAGGGAGCAGTCAGGCAAATATGAGTGCAAAGCTGC 578

Qy        745 CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATA 804

Db        579 CAACGAGGTCTCCTCGGCGGATGTCAAACAAGTCAAGGTCACTGTGAACTATCCTCCCAC 638
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Qy        805 CATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGA 864
Db        639 TATCACAGAATCCAAGAGCAATGAAGCCACCACAGGACGACAAGCTTCACTCAAATGTGA 698

Qy        865 AGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGA 924
Db        699 GGCCTCGGCAGTGCCTGCACCTGACTTTGAGTGGTACCGGGATGACACTAG---GATAAA 755

Qy        925 AGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAA 984
Db        756 TAGTGCCAATGGCCTTGAGATTAAGAGCACGGAGGGCCAGTCTTCCCTGACGGTGACCAA 815

Qy        985 TGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACAC 1044
Db        816 CGTCACTGAGGAGCACTACGGCAACTACACCTGTGTGGCTGCCAACAAGCTGGGGTCAC 875

Qy       1045 CAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCG 1085
Db        876 CAATGCCAGCCTAGTCCTTTTCAGACCTGGGTCGGTGAGAG 916
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RESULT 4
US-08-414-657D-1
; Sequence 1, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 977 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 2...976
; OTHER INFORMATION:
US-08-414-657D-1

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  Query Match             20.3%;  Score 340.6;  DB 2;  Length 977;
  Best Local Similarity   63.3%;  Pred. No. 9.8e-80;
  Matches  558;  Conservative    0;  Mismatches  314;  Indels    9;  Gaps    2;

Qy        205 TCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAA 264
Db         46 TCTTCCCACAGGACTGCCTGTTCGCAGCGTGGAT------TTTAACCGAGGCACGGACAA 99

Qy        265 CGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCAC 324
Db        100 CATCACCGTGAGGCAGGGGGACACAGCCATCCTCAGGTGCGTTCTAGAAGACAAGAACTC 159

Qy        325 CCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCT 384
Db        160 AAAGGTGGCCTGGTTGAACCGTTCTGGCATCATTTTTGCTGGACATGACAAGTGGTCTCT 219

Qy        385 GGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAA 444
Db        220 GGACCCACGGGTTGAGCTGGAGAAACGCCATTCTCTGGAATACAGCCTCCGAATCCAGAA 279

Qy        445 CGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAA 504
Db        280 GGTGGATGTCTATGATGAGGGTTCCTACACTTGCTCAGTTCAGACACAGCATGAGCCCAA 339

Qy        505 GACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGA 564
Db        340 GACCTCCCAAGTTTACTTGATCGTACAAGTCCCACCAAAGATCTCCAATATCTCCTCGGA 399

Qy        565 TATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGA 624
Db        400 TGTCACTGTGAATGAGGGCAGCAACGTGACTCTGGTCTGCATGGCCAATGGCCGTCCTGA 459

Qy        625 GCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGA 684
Db        460 ACCTGTTATCACCTGGAGACACCTTACACCAACTGGAAGGGAATTTGAAGGAGAAGAAGA 519

Qy        685 ATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC 744
Db        520 ATATCTGGAGATCCTTGGCATCACCAGGGAGCAGTCAGGCAAATATGAGTGCAAAGCTGC 579

Qy        745 CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATA 804
Db        580 CAACGAGGTCTCCTCGGCGGATGTCAAACAAGTCAAGGTCACTGTGAACTATCCTCCCAC 639

Qy        805 CATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGA 864
Db        640 TATCACAGAATCCAAGAGCAATGAAGCCACCACAGGACGACAAGCTTCACTCAAATGTGA 699

Qy        865 AGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGA 924
Db        700 GGCCTCGGCAGTGCCTGCACCTGACTTTGAGTGGTACCGGGATGACACTAG---GATAAA 756

Qy        925 AGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAA 984
Db        757 TAGTGCCAATGGCCTTGAGATTAAGAGCACGGAGGGCCAGTCTTCCCTGACGGTGACCAA 816

Qy        985 TGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACAC 1044
Db        817 CGTCACTGAGGAGCACTACGGCAACTACACCTGTGTGGCTGCCAACAAGCTGGGGTCAC 876

Qy       1045 CAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCG 1085
Db        877 CAATGCCAGCCTAGTCCTTTTCAGACCTGGGTCGGTGAGAG 917
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RESULT 5
US-09-135-080-1
; Sequence 1, Application US/09135080
; Patent No. 6423827
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat R.
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak

```
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/135,080
;      FILING DATE:  17-AUG-1998
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/414,657
;      FILING DATE:  31-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-620-3214
;      TELEFAX:  609-620-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  977 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  2...976
;      OTHER INFORMATION:
US-09-135-080-1

  Query Match           20.3%;  Score 340.6;  DB 4;  Length 977;
  Best Local Similarity   63.3%;  Pred. No. 9.8e-80;
  Matches  558;  Conservative    0;  Mismatches  314;  Indels    9;  Gaps    2;

Qy       205 TCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAA 264
            |||   |  |||| |||| || |||||||  |||      ||   |  ||  | ||||||
Db        46 TCTTCCCACAGGACTGCCTGTTCGCAGCGTGGAT------TTTAACCGAGGCACGGACAA 99

Qy       265 CGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCAC 324
            | | || ||  |||||||||| |  |||| ||||||||||  | | ||  || | | |
Db       100 CATCACCGTGAGGCAGGGGGACACAGCCATCCTCAGGTGCGTTCTAGAAGACAAGAACTC 159

Qy       325 CCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCT 384
               ||||||||| | |||||      |||| | | ||||||  ||||||||||||  ||
Db       160 AAAGGTGGCCTGGTTGAACCGTTCTGGCATCATTTTTGCTGGACATGACAAGTGGTCTCT 219

Qy       385 GGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAA 444
            ||| || || || |  ||   ||    |        | | ||||||  ||  ||||||||
Db       220 GGACCCACGGGTTGAGCTGGAGAAACGCCATTCTCTGGAATACAGCCTCCGAATCCAGAA 279

Qy       445 CGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAA 504
             |||||||| ||||| |||||  | ||||| ||||| || ||||||  |   |  | || ||
Db       280 GGTGGATGTCTATGATGAGGGTTCCTACACTTGCTCAGTTCAGACACAGCATGAGCCCAA 339

Qy       505 GACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGA 564
             ||||||   .||  || | || || ||||  | || || ||     | || || || ||
Db       340 GACCTCCCAAGTTTACTTGATCGTACAAGTCCCACCAAAGATCTCCAATATCTCCTCGGA 399

Qy       565 TATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGA 624
            | || |  | ||||| || | |||  | |  ||  |||||| || | |||  | || ||

Db       400 TGTCACTGTGAATGAGGGCAGCAACGTGACTCTGGTCTGCATGGCCAATGGCCGTCCTGA 459

Qy       625 GCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGA 684
               |||    | || |||||||||  |  | || |  |     |  ||||   | ||||| ||
Db       460 ACCTGTTATCACCTGGAGACACCTTACACCAACTGGAAGGGAATTTGAAGGAGAAGAAGA 519

Qy       685 ATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC 744
             |||  |||| || |  |||||||| ||||||||||||  | || |||||||  ||  |
Db       520 ATATCTGGAGATCCTTGGCATCACCAGGGAGCAGTCAGGCAAATATGAGTGCAAAGCTGC 579

Qy       745 CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATA 804
             ||| || ||  || || | |  ||      ||| |||||||| ||||||||||| ||
Db       580 CAACGAGGTCTCCTCGGCGGATGTCAAACAAGTCAAGGTCACTGTGAACTATCCTCCCAC 639

Qy       805 CATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGA 864
             ||  ||||| ||||| | |  |  | | ||   |||| | | |   ||||  | |||||
Db       640 TATCACAGAATCCAAGAGCAATGAAGCCACCACAGGACGACAAGCTTCACTCAAATGTGA 699

Qy       865 AGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGA 924
             ||||| ||||| ||  || | || ||  ||||||||  ||||||||  ||   ||| |
Db       700 GGCCTCGGCAGTGCCTGCACCTGACTTTGAGTGGTACCGGGATGACACTAG---GATAAA 756

Qy       925 AGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAA 984
               |    || ||  |  |  |  | | ||        ||  ||    || |   |  |||
Db       757 TAGTGCCAATGGCCTTGAGATTAAGAGCACGGAGGGCCAGTCTTCCCTGACGGTGACCAA 816

Qy       985 TGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACAC 1044
             ||| |||| .|  |||| || |||||||| || |||||  ||||||||||||   |||
Db       817 CGTCACTGAGGAGCACTACGGCAACTACACCTGTGTGGCTGCCAACAAGCTGGGGGTCAC 876

Qy      1045 CAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCG 1085
             |||||||||| |  | || ||  | || ||  | || || |
Db       877 CAATGCCAGCCTAGTCCTTTTCAGACCTGGGTCGGTGAGAG 917


RESULT 6
US-08-414-657D-5
; Sequence 5, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
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;     TELEX:
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1014 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     FEATURE:
;       NAME/KEY:  Coding Sequence
;       LOCATION:  1...1014
;       OTHER INFORMATION:
US-08-414-657D-5

  Query Match             20.3%;  Score 340.6;  DB 2;  Length 1014;
  Best Local Similarity   61.9%;  Pred. No. 1e-79;
  Matches  595;  Conservative    0;  Mismatches  354;  Indels   12;  Gaps    3;

Qy        205 TCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAA 264
              |||    |  |||| ||||||| |||||||  |||        ||   |  ||   | ||||||
Db         66 TCTTCCCACAGGACTGCCCGTTCGCAGCGTGGAT------TTTAACCGAGGCACGGACAA 119

Qy        265 CGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCAC 324
              | | || ||  |||||||||| |  |||| ||||||||        | ||  ||   |  | |
Db        120 CATCACCGTGAGGCAGGGGGACACGGCCATCCTCAGGTGTGTGGTAGAAGACAAGAACTC 179

Qy        325 CCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCT 384
              ||||||||| | ||||||       |||| |||  |||||  | |||||||||||  ||
Db        180 GAAAGTGGCCTGGTTGAACCGCTCTGGCATCATCTTCGCTGGACACGACAAGTGGTCTCT 239

Qy        385 GGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAA 444
              ||| ||||| || |  ||   ||     |           | | ||||||| ||   |||||||
Db        240 GGACCCTCGGGTTGAGCTGGAGAAACGCCATGCTCTGGAATACAGCCTCCGAATCCAGAA 299

Qy        445 CGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAA 504
              ||||||| ||||| || ||   | |||||  |||||| |||||| ||  ||||||   |   | || ||
Db        300 GGTGGATGTCTATGATGAAGGATCCTACACATGCTCAGTTCAGACACAGCATGAGCCCAA 359

Qy        505 GACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGA 564
              |||||||   ||  || |  ||||| |||||  | || || ||      | || || || ||
Db        360 GACCTCTCAAGTTTACTTGATTGTACAAGTTCCACCAAAGATCTCCAACATCTCCTCGGA 419

Qy        565 TATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGA 624
              | ||  |  | ||||| || |  | ||||  | |||     ||||||.|| |||  ||  |||
Db        420 TGTCACTGTGAATGAGGGCAGCAATGTAACCCTGGTCTGCATGGCCAATGGGCGCCCTGA 479

Qy        625 GCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGA 684
              |||      | || ||||||||| |  | ||       |        |   ||||    | ||||| ||
Db        480 ACCTGTTATCACCTGGAGACACCTTACACCACTTGGAAGAGAATTTGAAGGAGAAGAAGA 539

Qy        685 ATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC 744
              |||  |||| || |  ||||||||| ||||  ||||||||  | || ||||||   ||  |
Db        540 ATATCTGGAGATCCTAGGCATCACCAGGGAACAGTCAGGCAAATATGAGTGCAAGGCTGC 599

Qy        745 CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATA 804
              ||| || ||    || |  |  | | ||        ||| |||||||| ||||||||||||||
Db        600 CAACGAGGTCTCCTCCGCGGATGTCAAACAAGTCAAGGTCACTGTGAACTATCCACCCAC 659

Qy        805 CATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGA 864
              |||  ||||   | ||| |  |   |  |  | ||   |||| | | |      | || |  |||||
Db        660 CATCACAGAGTCTAAGAGCAATGAAGCCACCACAGGACGACAAGCTTCCCTCAAATGTGA 719

Qy        865 AGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGA 924
              ||||||||| || ||  || || ||  || ||||||||| |||||||  ||   |||  |
Db        720 AGCCTCAGCGGTGCCTGCACCTGACTTTGAGTGGTACCGGGATGACACCAG---GATAAA 776

Qy        925 AGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAA 984
                 |    || || |  |  |  |  | | ||      || ||     || |  |   ||
Db        777 CAGTGCAAACGGCCTTGAGATTAAGAGCACTGAGGGCCAGTCCTCCCTGACGGTGACCAA 836

Qy        985 TGTCTCTGAACATGACTATGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACAC 1044
              ||| ||||   |   |||| || ||||| || || |||||  |||||||||| |||  |||
Db        837 CGTCACTGAGGAACACTACGGCAACTATACCTGTGTGGCTGCCAACAAGCTCGGCGTCAC 896

Qy       1045 CAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTC 1104
              ||||||||||  |  | ||  || | |  ||  | || ||      |  | ||||||  |
Db        897 CAATGCCAGCCTAGTCCTTTTCAGACCCGGGTCGGTGAG---AGGAATCAACGGATCCAT 953

Qy       1105 GAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATT 1164
                ||  |||  |     | |||||||||| |        | ||   |||  ||   |||||
Db        954 CAGTCTGGCCGTACCACTGTGGCTGCTGGCAGCGTCCCTGTTCTGCCTTCTCAGCAAATG 1013

Qy       1165 T 1165
              |
Db       1014 T 1014

RESULT 7
US-09-135-080-7
; Sequence 7, Application US/09135080
; Patent No. 6423827
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat R.
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/135,080
;      FILING DATE:  17-AUG-1998
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/414,657
;      FILING DATE:  31-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-620-3214
;      TELEFAX:  609-620-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1014 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...1014
;      OTHER INFORMATION:
US-09-135-080-7

  Query Match             20.3%;  Score 340.6;  DB 4;  Length 1014;
  Best Local Similarity   61.9%;  Pred. No. 1e-79;
  Matches  595;  Conservative    0;  Mismatches  354;  Indels   12;  Gaps    3;

Qy        205 TCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAA 264
              |||    |  |||| ||||||| |||||||  |||        ||   |  ||   | ||||||
Db         66 TCTTCCCACAGGACTGCCCGTTCGCAGCGTGGAT------TTTAACCGAGGCACGGACAA 119

Qy        265 CGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCAC 324
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Db        120 CATCACCGTGAGGCAGGGGGACACGGCCATCCTCAGGTGTGTGGTAGAAGACAAGAACTC 179

Qy        325 CCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCT 384

Db        180 GAAAGTGGCCTGGTTGAACCGCTCTGGCATCATCTTCGCTGGACACGACAAGTGGTCTCT 239

Qy        385 GGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAA 444

Db        240 GGACCCTCGGGTTGAGCTGGAGAAACGCCATGCTCTGGAATACAGCCTCCGAATCCAGAA 299

Qy        445 CGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAA 504

Db        300 GGTGGATGTCTATGATGAAGGATCCTACACATGCTCAGTTCAGACACAGCATGAGCCCAA 359

Qy        505 GACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGA 564

Db        360 GACCTCTCAAGTTTACTTGATTGTACAAGTTCCACCAAAGATCTCCAACATCTCCTCGGA 419

Qy        565 TATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGA 624

Db        420 TGTCACTGTGAATGAGGGCAGCAATGTAACCCTGGTCTGCATGGCCAATGGGCGCCCTGA 479

Qy        625 GCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGA 684

Db        480 ACCTGTTATCACCTGGAGACACCTTACACCACTTGGAAGAGAATTTGAAGGAGAAGAAGA 539

Qy        685 ATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC 744

Db        540 ATATCTGGAGATCCTAGGCATCACCAGGGAACAGTCAGGCAAATATGAGTGCAAGGCTGC 599

Qy        745 CAATGACGTGGCCGCGCCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATA 804

Db        600 CAACGAGGTCTCCTCCGCGGATGTCAAACAAGTCAAGGTCACTGTGAACTATCCACCCAC 659

Qy        805 CATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGA 864

Db        660 CATCACAGAGTCTAAGAGCAATGAAGCCACCACAGGACGACAAGCTTCCCTCAAATGTGA 719

Qy        865 AGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGA 924

Db        720 AGCCTCAGCGGTGCCTGCACCTGACTTTGAGTGGTACCGGGATGACACCAG---GATAAA 776

Qy        925 AGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAA 984

Db        777 CAGTGCAAACGGCCTTGAGATTAAGAGCACTGAGGGCCAGTCCTCCCTGACGGTGACCAA 836

Qy        985 TGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACAC 1044

Db        837 CGTCACTGAGGAACACTACGGCAACTATACCTGTGTGGCTGCCAACAAGCTCGGCGTCAC 896

Qy       1045 CAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTC 1104

Db        897 CAATGCCAGCCTAGTCCTTTTCAGACCCGGGTCGGTGAG---AGGAATCAACGGATCCAT 953

Qy       1105 GAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATT 1164

Db        954 CAGTCTGGCCGTACCACTGTGGCTGCTGGCAGCGTCCCTGTTCTGCCTTCTCAGCAAATG 1013

Qy       1165 T 1165
              |
Db       1014 T 1014
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RESULT 8
US-08-414-657D-9
; Sequence 9, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  861 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...861
;      OTHER INFORMATION:
US-08-414-657D-9

  Query Match           20.2%;  Score 338.6;  DB 2;  Length 861;
  Best Local Similarity  63.7%;  Pred. No. 3.1e-79;
  Matches  531;  Conservative    0;  Mismatches  299;  Indels    3;  Gaps    1;

Qy        253 AGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGA 312

Db         24 AGGCACGGACAACATCACCGTGAGGCAGGGGGACACAGCCATCCTCAGGTGCGTTCTAGA 83

Qy        313 CAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA 372

Db         84 AGACAAGAACTCAAAGGTGGCCTGGTTGAACCGTTCTGGCATCATTTTTGCTGGACATGA 143

Qy        373 CAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCAT 432

Db        144 CAAGTGGTCTCTGGACCCACGGGTTGAGCTGGAGAAACGCCATTCTCTGGAATACAGCCT 203

Qy        433 CGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGA 492

Db        204 CCGAATCCAGAAGGTGGATGTCTATGATGAGGGTTCCTACACTTGCTCAGTTCAGACACA 263

Qy        493 CAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGA 552

Db        264 GCATGAGCCCAAGACCTCCCAAGTTTACTTGATCGTACAAGTCCCACCAAAGATCTCCAA 323

Qy        553 GATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAAC 612

Db        324 TATCTCCTCGGATGTCACTGTGAATGAGGGCAGCAACGTGACTCTGGTCTGCATGGCCAA 383

Qy        613 TGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGT 672

Db        384 TGGCCGTCCTGAACCTGTTATCACCTGGAGACACCTTACACCAACTGGAAGGGAATTTGA 443
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Qy        673 GAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGA 732
              | ||||| ||||||  |||| || |  |||||||| ||||||||||||  | || ||
Db        444 AGGAGAAGAAGAATATCTGGAGATCCTTGGCATCACCAGGGAGCAGTCAGGCAAATATGA 503

Qy        733 GTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAA 792
              |||||  ||  |||| || ||  || || | |  ||       ||| |||||||| |||||
Db        504 GTGCAAAGCTGCCAACGAGGTCTCCTCGGCGGATGTCAAACAAGTCAAGGTCACTGTGAA 563

Qy        793 CTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGAC 852
              |||||| ||    ||  ||||| ||||| | |  |  | | ||   |||| | | |   |
Db        564 CTATCCTCCCACTATCACAGAATCCAAGAGCAATGAAGCCACCACAGGACGACAAGCTTC 623

Qy        853 ACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAA 912
              |||  | |||||  |||||  |||||  ||  || | ||  ||  ||||||||  ||||||||
Db        624 ACTCAAATGTGAGGCCTCGGCAGTGCCTGCACCTGACTTTGAGTGGTACCGGGATGACAC 683

Qy        913 AAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACT 972
              ||   |||  |  |    || ||  |  |  |  | | ||       ||  ||    ||
Db        684 TAG---GATAAATAGTGCCAATGGCCTTGAGATTAAGAGCACGGAGGGCCAGTCTTCCCT 740

Qy        973 CATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAA 1032
              |   |   ||| ||| ||||  |  |||| || |||||||| || |||||  |||||||
Db        741 GACGGTGACCAACGTCACTGAGGAGCACTACGGCAACTACACCTGTGTGGCTGCCAACAA 800

Qy       1033 GCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCG 1085
              ||||||  |||||||||||||| |  | || ||  | || ||  | || || |
Db        801 GCTGGGGGTCACCAATGCCAGCCTAGTCCTTTTCAGACCTGGGTCGGTGAGAG 853


RESULT 9
US-08-414-657D-6
; Sequence 6, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  912 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1..912
;      OTHER INFORMATION:
US-08-414-657D-6

  Query Match           20.2%;  Score 338.6;  DB 2;  Length 912;
  Best Local Similarity  63.7%;  Pred. No. 3.2e-79;
  Matches  531;  Conservative    0;  Mismatches  299;  Indels    3;  Gaps    1;

Qy        253 AGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGA 312
              ||  | |||||| | ||  ||  |||||||||| |  |||| |||||||||  | | ||
Db         24 AGGCACGGACAACATCACCGTGAGGCAGGGGGACACAGCCATCCTCAGGTGCGTTCTAGA 83

Qy        313 CAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA 372
              ||  |  | |  ||||||||||| | |||||      |||| | | ||||||  ||||
Db         84 AGACAAGAACTCAAAGGTGGCCTGGTTGAACCGTTCTGGCATCATTTTTGCTGGACATGA 143

Qy        373 CAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCAT 432
              |||||||| |||||  || || || |  ||  ||    |       | | |||||| |
Db        144 CAAGTGGTCTCTGGACCCACGGGTTGAGCTGGAGAAACGCCATTCTCTGGAATACAGCCT 203

Qy        433 CGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGA 492
              |  |||||||| |||||||| |||||  |||||  | |||||  |||||  || |||||| |
Db        204 CCGAATCCAGAAGGTGGATGTCTATGATGAGGGTTCCTACACTTGCTCAGTTCAGACACA 263

Qy        493 CAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGA 552
              |  | || ||||||||    ||  || | || || |||||  | || || ||     |
Db        264 GCATGAGCCCAAGACCTCCCAAGTTTACTTGATCGTACAAGTCCCACCAAAGATCTCCAA 323

Qy        553 GATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAAC 612
              || || || ||| || |  | |||||  || | |||  | |  ||   ||||||  || |
Db        324 TATCTCCTCGGATGTCACTGTGAATGAGGGCAGCAACGTGACTCTGGTCTGCATGGCCAA 383

Qy        613 TGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGT 672
              |||  | || || |||    | || |||||||||  |  | || |  |    |  ||||
Db        384 TGGCCGTCCTGAACCTGTTATCACCTGGAGACACCTTACACCAACTGGAAGGGAATTTGA 443

Qy        673 GAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGA 732
              | ||||| ||||| |||| || |  |||||||| ||||||||||||  | || ||
Db        444 AGGAGAAGAAGAATATCTGGAGATCCTTGGCATCACCAGGGAGCAGTCAGGCAAATATGA 503

Qy        733 GTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAA 792
              |||||  ||  |||| || ||  || || | |  ||       ||| |||||||| |||||
Db        504 GTGCAAAGCTGCCAACGAGGTCTCCTCGGCGGATGTCAAACAAGTCAAGGTCACTGTGAA 563

Qy        793 CTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGAC 852
              |||||| ||    ||  ||||| ||||| | |  |  | | ||   |||| | | |   |
Db        564 CTATCCTCCCACTATCACAGAATCCAAGAGCAATGAAGCCACCACAGGACGACAAGCTTC 623

Qy        853 ACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAA 912
              |||  | |||||  |||||  |||||  ||  || | ||  ||  ||||||||  ||||||||
Db        624 ACTCAAATGTGAGGCCTCGGCAGTGCCTGCACCTGACTTTGAGTGGTACCGGGATGACAC 683

Qy        913 AAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACT 972
              ||   |||  |  |    || ||  |  |  |  | | ||       ||  ||    ||
Db        684 TAG---GATAAATAGTGCCAATGGCCTTGAGATTAAGAGCACGGAGGGCCAGTCTTCCCT 740

Qy        973 CATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAA 1032
              |   |   ||| ||| ||||  |  |||| || |||||||| || |||||  |||||||
Db        741 GACGGTGACCAACGTCACTGAGGAGCACTACGGCAACTACACCTGTGTGGCTGCCAACAA 800

Qy       1033 GCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCG 1085
              ||||||  |||||||||||||| |  | || ||  | || ||  | || || |
Db        801 GCTGGGGGTCACCAATGCCAGCCTAGTCCTTTTCAGACCTGGGTCGGTGAGAG 853


RESULT 10
US-08-414-657D-8
; Sequence 8, Application US/08414657D
; Patent No. 5861283
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;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  945 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1..945
;      OTHER INFORMATION:
US-08-414-657D-8

  Query Match          20.1%;  Score 337.4;  DB 2;  Length 945;
  Best Local Similarity   63.1%;  Pred. No. 6.7e-79;
  Matches  556;  Conservative    0;  Mismatches  316;  Indels    9;  Gaps    2;

Qy        205 TCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAA 264
              |||   | ||||  |||||||  |||||||  |||     ||    |  ||  | ||||||
Db         66 TCTTCCCACAGGACTGCCCGTTCGCAGCGTGGAT------TTTAACCGAGGCACGGACAA 119

Qy        265 CGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCAC 324
              | | || ||  ||||||||||  |  ||||  |||||||||      | ||  ||  |  | |
Db        120 CATCACCGTGAGGCAGGGGGACACGGCCATCCTCAGGTGTGTGGTAGAAGACAAGAACTC 179

Qy        325 CCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCT 384
                |||||||||  | ||||||     |||| |||  |||||  | ||||||||||  ||
Db        180 GAAAGTGGCCTGGTTGAACCGCTCTGGCATCATCTTCGCTGGACACGACAAGTGGTCTCT 239

Qy        385 GGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAA 444
              |||  |||||  ||  |  ||   ||     |        | |  ||||||  ||   ||||||||
Db        240 GGACCCTCGGGTTGAGCTGGAGAAACGCCATGCTCTGGAATACAGCCTCCGAATCCAGAA 299

Qy        445 CGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAA 504
                |||||||| |||||  || ||   | |||||  |||||  ||  ||||||  |  |  | || ||
Db        300 GGTGGATGTCTATGATGAAGGATCCTACACATGCTCAGTTCAGACACAGCATGAGCCCAA 359

Qy        505 GACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGA 564
              |||||||  :  ||   ||  |  |||||  |||||   |  ||  ||  ||      |  ||  ||  ||  ||

Db        360 GACCTCTCAAGTTTACTTGATTGTACAAGTTCCACCAAAGATCTCCAACATCTCCTCGGA 419

Qy        565 TATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGA 624
              |  ||  |  |||||  ||  |  ||||  |  |  |||    ||||||  ||  |||||   |  ||  ||
Db        420 TGTCACTGTGAATGAGGGCAGCAATGTAACCCTGGTCTGCATGGCCAATGGGCGCCCTGA 479

Qy        625 GCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGA 684
                |||    |  ||  ||||||||||  |  |  ||      |       |  ||||    | |||||  ||
Db        480 ACCTGTTATCACCTGGAGACACCTTACACCACTTGGAAGAGAATTTGAAGGAGAAGAAGA 539

Qy        685 ATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC 744
              |||  ||||  ||  |  ||||||||||  ||||  ||||||||   |  ||  |||||||   ||  |
Db        540 ATATCTGGAGATCCTAGGCATCACCAGGGAACAGTCAGGCAAATATGAGTGCAAGGCTGC 599

Qy        745 CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATA 804
              |||  ||  ||   ||  |  |  |  ||       |||  ||||||||  ||||||||||||||
Db        600 CAACGAGGTCTCCTCCGCGGATGTCAAACAAGTCAAGGTCACTGTGAACTATCCACCCAC 659

Qy        805 CATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGA 864
              |||  ||||  | |||  |  |  |  |  |  ||   ||||  |  |  |   |  ||  | |||||
Db        660 CATCACAGAGTCTAAGAGCAATGAAGCCACCACAGGACGACAAGCTTCCCTCAAATGTGA 719

Qy        865 AGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGA 924
              |||||||||  ||  ||   ||  |  ||  ||  ||||||||   ||||||||   ||   |||  |
Db        720 AGCCTCAGCGGTGCCTGCACCTGACTTTGAGTGGTACCGGGATGACACCAG---GATAAA 776

Qy        925 AGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAA 984
                |    ||  ||  |  |  |  |  |  ||        ||  ||    ||  |    |   |||
Db        777 CAGTGCAAACGGCCTTGAGATTAAGAGCACTGAGGGCCAGTCCTCCCTGACGGTGACCAA 836

Qy        985 TGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACAC 1044
              |||  ||||  |  ||||  ||  ||||||  ||  ||  ||||||  ||||||||||  |||  |||
Db        837 CGTCACTGAGGAACACTACGGCAACTATACCTGTGTGGCTGCCAACAAGCTCGGCGTCAC 896

Qy       1045 CAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCG 1085
              ||||||||||  |  ||  ||  |  ||  ||  |  ||  || |
Db        897 CAATGCCAGCCTAGTCCTTTTCAGACCCGGGTCGGTGAGAG 937


RESULT 11
US-08-414-657D-10
; Sequence 10, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
```

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;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  861 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...861
;      OTHER INFORMATION:
US-08-414-657D-10

  Query Match           19.9%;  Score 333.8;  DB 2;  Length 861;
  Best Local Similarity  63.4%;  Pred. No. 5.6e-78;
  Matches  528;  Conservative    0;  Mismatches  302;  Indels    3;  Gaps    1;

Qy       253 AGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGA 312
Db        24 AGGCACGGACAACATCACCGTGAGGCAGGGGGACACGGCCATCCTCAGGTGTGTGGTAGA 83

Qy       313 CAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA 372
Db        84 AGACAAGAACTCGAAAGTGGCCTGGTTGAACCGCTCTGGCATCATCTTCGCTGGACACGA 143

Qy       373 CAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCAT 432
Db       144 CAAGTGGTCTCTGGACCCTCGGGTTGAGCTGGAGAAACGCCATGCTCTGGAATACAGCCT 203

Qy       433 CGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGA 492
Db       204 CCGAATCCAGAAGGTGGATGTCTATGATGAAGGATCCTACACATGCTCAGTTCAGACACA 263

Qy       493 CAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGA 552
Db       264 GCATGAGCCCAAGACCTCTCAAGTTTACTTGATTGTACAAGTTCCACCAAAGATCTCCAA 323

Qy       553 GATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAAC 612
Db       324 CATCTCCTCGGATGTCACTGTGAATGAGGGCAGCAATGTAACCCTGGTCTGCATGGCCAA 383

Qy       613 TGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGT 672
Db       384 TGGGCGCCCTGAACCTGTTATCACCTGGAGACACCTTACACCACTTGGAAGAGAATTTGA 443

Qy       673 GAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGA 732
Db       444 AGGAGAAGAAGAATATCTGGAGATCCTAGGCATCACCAGGGAACAGTCAGGCAAATATGA 503

Qy       733 GTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAA 792
Db       504 GTGCAAGGCTGCCAACGAGGTCTCCTCCGCGGATGTCAAACAAGTCAAGGTCACTGTGAA 563

Qy       793 CTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGAC 852
Db       564 CTATCCACCCACCATCACAGAGTCTAAGAGCAATGAAGCCACCACAGGACGACAAGCTTC 623

Qy       853 ACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAA 912
Db       624 CCTCAAATGTGAAGCCTCAGCGGTGCCTGCACCTGACTTTGAGTGGTACCGGGATGACAC 683

Qy       913 AAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACT 972
Db       684 CAG---GATAAACAGTGCAAACGGCCTTGAGATTAAGAGCACTGAGGGCCAGTCCTCCCT 740

Qy       973 CATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAA 1032
Db       741 GACGGTGACCAACGTCACTGAGGAACACTACGGCAACTATACCTGTGTGGCTGCCAACAA 800

Qy      1033 GCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCG 1085
Db       801 GCTCGGCGTCACCAATGCCAGCCTAGTCCTTTTCAGACCCGGGTCGGTGAGAG 853


RESULT 12
US-08-414-657D-17
; Sequence 17, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  756 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...756
;      OTHER INFORMATION:
US-08-414-657D-17

  Query Match           18.1%;  Score 303.6;  DB 2;  Length 756;
  Best Local Similarity  63.5%;  Pred. No. 4.4e-70;
  Matches  481;  Conservative    0;  Mismatches  274;  Indels    3;  Gaps    1;

Qy       281 GGGGACAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTA 340
Db         1 GGGGACACAGCCATCCTCAGGTGCGTTCTAGAAGACAAGAACTCAAAGGTGGCCTGGTTG 60

Qy       341 AACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTC 400
Db        61 AACCGTTCTGGCATCATTTTTGCTGGACATGACAAGTGGTCTCTGGACCCACGGGTTGAG 120

Qy       401 CTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGAC 460
Db       121 CTGGAGAAACGCCATTCTCTGGAATACAGCCTCCGAATCCAGAAGGTGGATGTCTATGAT 180

Qy       461 GAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCAC 520
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Db        181 GAGGGTTCCTACACTTGCTCAGTTCAGACACAGCATGAGCCCAAGACCTCCCAAGTTTAC 240

Qy        521 CTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAA 580

Db        241 TTGATCGTACAAGTCCCACCAAAGATCTCCAATATCTCCTCGGATGTCACTGTGAATGAG 300

Qy        581 GGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGG 640

Db        301 GGCAGCAACGTGACTCTGGTCTGCATGGCCAATGGCCGTCCTGAACCTGTTATCACCTGG 360

Qy        641 AGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAG 700

Db        361 AGACACCTTACACCAACTGGAAGGGAATTTGAAGGAGAAGAAGAATATCTGGAGATCCTT 420

Qy        701 GGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCG 760

Db        421 GGCATCACCAGGGAGCAGTCAGGCAAATATGAGTGCAAAGCTGCCAACGAGGTCTCCTCG 480

Qy        761 CCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAG 820

Db        481 GCGGATGTCAAACAAGTCAAGGTCACTGTGAACTATCCTCCCACTATCACAGAATCCAAG 540

Qy        821 GGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCC 880

Db        541 AGCAATGAAGCCACCACAGGACGACAAGCTTCACTCAAATGTGAGGCCTCGGCAGTGCCT 600

Qy        881 TCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTG 940

Db        601 GCACCTGACTTTGAGTGGTACCGGGATGACACTAG---GATAAATAGTGCCAATGGCCTT 657

Qy        941 AAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGAC 1000

Db        658 GAGATTAAGAGCACGGAGGGCCAGTCTTCCCTGACGGTGACCAACGTCACTGAGGAGCAC 717

Qy       1001 TATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGG 1038

Db        718 TACGGCAACTACACCTGTGTGGCTGCCAACAAGCTGGG 755


RESULT 13
US-08-414-657D-18
; Sequence 18, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  756 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...756
;      OTHER INFORMATION:
US-08-414-657D-18

  Query Match           17.8%;  Score 298.2;  DB 2;  Length 756;
  Best Local Similarity  63.0%;  Pred. No. 1.2e-68;
  Matches  478;  Conservative    0;  Mismatches  278;  Indels    3;  Gaps    1;

Qy        281 GGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTA 340

Db          1 GGGGACACGGCCATCCTCAGGTGTGTGGTAGAAGACAAGAACTCGAAAGTGGCCTGGTTG 60

Qy        341 AACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTC 400

Db         61 AACCGCTCTGGCATCATCTTCGCTGGACACGACAAGTGGTCTCTGGACCCTCGGGTTGAG 120

Qy        401 CTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGAC 460

Db        121 CTGGAGAAACGCCATGCTCTGGAATACAGCCTCCGAATCCAGAAGGTGGATGTCTATGAT 180

Qy        461 GAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCAC 520

Db        181 GAAGGATCCTACACATGCTCAGTTCAGACACAGCATGAGCCCAAGACCTCTCAAGTTTAC 240

Qy        521 CTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAA 580

Db        241 TTGATTGTACAAGTTCCACCAAAGATCTCCAACATCTCCTCGGATGTCACTGTGAATGAG 300

Qy        581 GGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGG 640

Db        301 GGCAGCAATGTAACCCTGGTCTGCATGGCCAATGGGCGCCCTGAACCTGTTATCACCTGG 360

Qy        641 AGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAG 700

Db        361 AGACACCTTACACCACTTGGAAGAGAATTTGAAGGAGAAGAAGAATATCTGGAGATCCTA 420

Qy        701 GGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCG 760

Db        421 GGCATCACCAGGGAACAGTCAGGCAAATATGAGTGCAAGGCTGCCAACGAGGTCTCCTCC 480

Qy        761 CCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAG 820

Db        481 GCGGATGTCAAACAAGTCAAGGTCACTGTGAACTATCCACCCACCATCACAGAGTCTAAG 540

Qy        821 GGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCC 880

Db        541 AGCAATGAAGCCACCACAGGACGACAAGCTTCCCTCAAATGTGAAGCCTCAGCGGTGCCT 600

Qy        881 TCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTG 940

Db        601 GCACCTGACTTTGAGTGGTACCGGGATGACACCAG---GATAAACAGTGCAAACGGCCTT 657

Qy        941 AAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGAC 1000

Db        658 GAGATTAAGAGCACTGAGGGCCAGTCCTCCCTGACGGTGACCAACGTCACTGAGGAACAC 717

Qy       1001 TATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGC 1039

Db        718 TACGGCAACTATACCTGTGTGGCTGCCAACAAGCTCGGC 756
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RESULT 14
US-08-414-657D-11
; Sequence 11, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  219 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...219
;      OTHER INFORMATION:
US-08-414-657D-11

  Query Match           6.0%;  Score 100;  DB 2;  Length 219;
  Best Local Similarity   67.0%;  Pred. No. 6.3e-17;
  Matches  142;  Conservative    0;  Mismatches   70;  Indels    0;  Gaps    0;

Qy        281 GGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTA 340
              ||||| |  |||| |||||||||||  | | ||  ||  |  | |   |||||||||| |
Db          1 GGGGACACAGCCATCCTCAGGTGCGTTCTAGAAGACAAGAACTCAAAGGTGGCCTGGTTG 60

Qy        341 AACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTC 400
              |||||      |||| | | |||||| ||||||||||||  ||||| || || || |
Db         61 AACCGTTCTGGCATCATTTTTGCTGGACATGACAAGTGGTCTCTGGACCCACGGGTTGAG 120

Qy        401 CTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGAC 460
              ||   ||    |      | | |||||| ||   |||||||| |||||||| |||||
Db        121 CTGGAGAAACGCCATTCTCTGGAATACAGCCTCCGAATCCAGAAGGTGGATGTCTATGAT 180

Qy        461 GAGGGCCCTTACACCTGCTCGGTGCAGACAGA 492
              |||||  | ||||| ||||| || |||||| |
Db        181 GAGGGTTCCTACACTTGCTCAGTTCAGACACA 212
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RESULT 15
US-08-414-657D-12
; Sequence 12, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  219 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...219
;      OTHER INFORMATION:
US-08-414-657D-12

  Query Match           5.7%;  Score 95.2;  DB 2;  Length 219;
  Best Local Similarity   65.6%;  Pred. No. 1.1e-15;
  Matches  139;  Conservative    0;  Mismatches   73;  Indels    0;  Gaps    0;

Qy        281 GGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTA 340
              ||||| |  |||| |||||||||     | ||  ||  |  | |   |||||||||| |
Db          1 GGGGACACGGCCATCCTCAGGTGTGTGGTAGAAGACAAGAACTCGAAAGTGGCCTGGTTG 60

Qy        341 AACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTC 400
              ||||||      |||| |||  |||||  | ||||||||||  ||||| ||||| || |
Db         61 AACCGCTCTGGCATCATCTTCGCTGGACACGACAAGTGGTCTCTGGACCCTCGGGTTGAG 120

Qy        401 CTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGAC 460
              ||   ||    |        | | |||||| ||   |||||||| |||||||| |||||
Db        121 CTGGAGAAACGCCATGCTCTGGAATACAGCCTCCGAATCCAGAAGGTGGATGTCTATGAT 180

Qy        461 GAGGGCCCTTACACCTGCTCGGTGCAGACAGA 492
              || ||  | ||||| ||||| || |||||| |
Db        181 GAAGGATCCTACACATGCTCAGTTCAGACACA 212
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Search completed: September 11, 2003, 02:51:42
Job time : 157 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 11, 2003, 01:36:43 ; Search time 568 Seconds
(without alignments)
7176.413 Million cell updates/sec

Title: US-10-017-084A-522
Perfect score: 1679
Sequence: 1 gttgtgtccttcagcaaaac.....ataaaaagagcaaaaaaaaa 1679

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 3264840

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1679	100.0	1679	10	US-09-999-832A-522	Sequence 522, App
5	1679	100.0	1679	11	US-09-978-189-522	Sequence 522, App
6	1679	100.0	1679	11	US-09-978-608A-522	Sequence 522, App
7	1679	100.0	1679	11	US-09-978-585A-522	Sequence 522, App
8	1679	100.0	1679	11	US-09-978-191A-522	Sequence 522, App
9	1679	100.0	1679	11	US-09-978-403A-522	Sequence 522, App
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ALIGNMENTS

RESULT 1
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; Sequence 522, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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RESULT 2
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; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
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; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Kuo, Sophia S.
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C27
; CURRENT APPLICATION NUMBER: US/09/978,697
; CURRENT FILING DATE: 2001-10-16
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; PRIOR FILING DATE: 2001-07-30
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

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RESULT 3
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
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; APPLICANT: Tumas, Daniel
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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C9
; CURRENT APPLICATION NUMBER: US/09/978,192A
; CURRENT FILING DATE: 2001-10-15
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60
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Db          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60

Qy         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120
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Db         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120

Qy        121 AAGAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180
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Db        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCCGTGCGCAGCGGAGATGC 240

Qy        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300
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Qy        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
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Db        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360

Qy        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420
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Qy        421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
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Db        481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540

Qy        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
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Db        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600

Qy        601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660
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Qy        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
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Db        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720

Qy        721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCCGTGGTACGGAGAGTAAA 780
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Db        721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCCGTGGTACGGAGAGTAAA 780

Qy        781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840
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Db        781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840

Qy        841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900
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Qy        961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020
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Qy       1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080
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Db       1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080

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Db       1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140

Qy       1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200
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Db       1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200

Qy       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
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Db       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260

Qy       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320
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Db       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320

Qy       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380
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Db       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380

Qy       1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440
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Qy       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
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RESULT 4
US-09-999-832A-522
; Sequence 522, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C63
;  CURRENT APPLICATION NUMBER: US/09/999,832A
;  CURRENT FILING DATE:  2001-10-24
;  PRIOR APPLICATION NUMBER: 09/918585
;  PRIOR FILING DATE: 2001-07-30
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
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;  PRIOR FILING DATE: 1997-11-03
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;  PRIOR APPLICATION NUMBER: 60/066364
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;  PRIOR FILING DATE: 1998-04-01
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60
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Qy         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120
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Qy      601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660
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Db      781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840

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Db     1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200

Qy     1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260

Qy     1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320

Qy     1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380

Qy     1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440

Qy     1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500

Qy     1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560

Qy     1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620

Qy     1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAAGAGCAAAAAAAAA 1679
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAAGAGCAAAAAAAAA 1679
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RESULT 5
US-09-978-189-522
; Sequence 522, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C7
;  CURRENT APPLICATION NUMBER: US/09/978,189
;  CURRENT FILING DATE:  2001-10-15
;  PRIOR APPLICATION NUMBER: 09/918585
;  PRIOR FILING DATE: 2001-07-30
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/064249
;  PRIOR FILING DATE: 1997-11-03
;  PRIOR APPLICATION NUMBER: 60/065311
;  PRIOR FILING DATE: 1997-11-13
;  PRIOR APPLICATION NUMBER: 60/066364
;  PRIOR FILING DATE: 1997-11-21
;  PRIOR APPLICATION NUMBER: 60/077450
;  PRIOR FILING DATE: 1998-03-10
;  PRIOR APPLICATION NUMBER: 60/077632
;  PRIOR FILING DATE: 1998-03-11
;  PRIOR APPLICATION NUMBER: 60/077641
;  PRIOR FILING DATE: 1998-03-11
;  PRIOR APPLICATION NUMBER: 60/077649
;  PRIOR FILING DATE: 1998-03-11
;  PRIOR APPLICATION NUMBER: 60/077791
;  PRIOR FILING DATE: 1998-03-12
;  PRIOR APPLICATION NUMBER: 60/078004
;  PRIOR FILING DATE: 1998-03-13
;  PRIOR APPLICATION NUMBER: 60/078886
;  PRIOR FILING DATE: 1998-03-20
;  PRIOR APPLICATION NUMBER: 60/078936
;  PRIOR FILING DATE: 1998-03-20
;  PRIOR APPLICATION NUMBER: 60/078910
;  PRIOR FILING DATE: 1998-03-20
;  PRIOR APPLICATION NUMBER: 60/078939
;  PRIOR FILING DATE: 1998-03-20
;  PRIOR APPLICATION NUMBER: 60/079294
;  PRIOR FILING DATE: 1998-03-25
;  PRIOR APPLICATION NUMBER: 60/079656
;  PRIOR FILING DATE: 1998-03-26
;  PRIOR APPLICATION NUMBER: 60/079664
;  PRIOR FILING DATE: 1998-03-27
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  Best Local Similarity   100.0%;  Pred. No. 1.7e-150;
  Matches  344;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60

Qy         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120

Qy        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180

Qy        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240

Qy        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300

Qy        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
              |||||||||||||||||||||||||||||||||||||||||||||
Db        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344


RESULT 7
US-09-978-585A-523
; Sequence 523, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C15
;  CURRENT APPLICATION NUMBER: US/09/978,585A
;  CURRENT FILING DATE:  2001-10-16
;  NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 523
;   LENGTH: 344
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-978-585A-523
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  Query Match           100.0%;  Score 1806;  DB 11;  Length 344;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-150;
  Matches  344;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60

Qy         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120

Qy        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180

Qy        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240

Qy        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300

Qy        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
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Db        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344


RESULT 8
US-09-978-191A-523
; Sequence 523, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C4
;  CURRENT APPLICATION NUMBER: US/09/978,191A
;  CURRENT FILING DATE:  2001-10-15
;  PRIOR APPLICATION NUMBER: 09/918585
;  PRIOR FILING DATE: 2001-07-30
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/064249
;  PRIOR FILING DATE: 1997-11-03
;  PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082796
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: 60/083336
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083392
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083554
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083558
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083500
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-5-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1806; DB 11; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.7e-150;

Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60

Qy         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120

Qy        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180

Qy        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240
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Db        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240

Qy        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300

Qy        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
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Db        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
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RESULT 6
US-09-978-608A-523
; Sequence 523, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 523
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-608A-523

Query Match 100.0%; Score 1806; DB 11; Length 344;

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Qy        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240
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Db        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240

Qy        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300

Qy        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
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Db        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344


RESULT 5
US-09-978-189-523
; Sequence 523, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C7
;  CURRENT APPLICATION NUMBER: US/09/978,189
;  CURRENT FILING DATE:  2001-10-15
;  PRIOR APPLICATION NUMBER: 09/918585
;  PRIOR FILING DATE: 2001-07-30
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/064249
;  PRIOR FILING DATE: 1997-11-03
;  PRIOR APPLICATION NUMBER: 60/065311
;  PRIOR FILING DATE: 1997-11-13
;  PRIOR APPLICATION NUMBER: 60/066364
;  PRIOR FILING DATE: 1997-11-21
;  PRIOR APPLICATION NUMBER: 60/077450
;  PRIOR FILING DATE: 1998-03-10
;  PRIOR APPLICATION NUMBER: 60/077632
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;  PRIOR APPLICATION NUMBER: 60/077641
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Query Match 100.0%; Score 1806; DB 10; Length 344;
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Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Query Match 100.0%; Score 1806; DB 10; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.7e-150;
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C63
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; TITLE OF INVENTION: Acids Encoding the Same
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; PRIOR APPLICATION NUMBER: 60/085697

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RESULT 3
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; Patent No. US20020177553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen

; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
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; PRIOR APPLICATION NUMBER: 60/085582
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; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1806; DB 10; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.7e-150;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
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; APPLICANT: Gao, Wei-Qiang
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; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
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; TITLE OF INVENTION: Acids Encoding the Same
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GenCore version 5.1.6

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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6	1806	100.0	344	11	US-09-978-608A-523	Sequence 523, App
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22	1806	100.0	344	12	US-09-978-188A-523	Sequence 523, App
23	1806	100.0	344	12	US-09-978-298A-523	Sequence 523, App
24	1806	100.0	344	12	US-10-137-870-376	Sequence 376, App
25	1806	100.0	344	12	US-10-140-018-376	Sequence 376, App
26	1806	100.0	344	12	US-10-140-021-376	Sequence 376, App
27	1806	100.0	344	12	US-10-140-274-376	Sequence 376, App
28	1806	100.0	344	12	US-10-140-471-376	Sequence 376, App
29	1806	100.0	344	12	US-10-140-807-376	Sequence 376, App
30	1806	100.0	344	12	US-10-140-922-376	Sequence 376, App
31	1806	100.0	344	12	US-10-140-924-376	Sequence 376, App
32	1806	100.0	344	12	US-10-140-926-376	Sequence 376, App
33	1806	100.0	344	12	US-10-141-698-376	Sequence 376, App
34	1806	100.0	344	12	US-10-141-702-376	Sequence 376, App
35	1806	100.0	344	12	US-10-141-704-376	Sequence 376, App
36	1806	100.0	344	12	US-10-142-421-376	Sequence 376, App
37	1806	100.0	344	12	US-10-142-432-376	Sequence 376, App
38	1806	100.0	344	12	US-10-142-767-376	Sequence 376, App
39	1806	100.0	344	12	US-10-143-031A-523	Sequence 523, App
40	1806	100.0	344	12	US-10-143-033-376	Sequence 376, App
41	1806	100.0	344	12	US-10-144-994-376	Sequence 376, App
42	1806	100.0	344	12	US-10-145-628-376	Sequence 376, App
43	1806	100.0	344	12	US-10-145-631-376	Sequence 376, App
44	1806	100.0	344	12	US-10-145-633-376	Sequence 376, App
45	1806	100.0	344	12	US-10-145-746-376	Sequence 376, App

ALIGNMENTS

RESULT 1
US-09-978-295A-523
; Sequence 523, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 252 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-414-657D-56

Query Match 44.1%; Score 796.5; DB 2; Length 252;
Best Local Similarity 56.9%; Pred. No. 1.3e-71;
Matches 144; Conservative 50; Mismatches 58; Indels 1; Gaps 1;

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              |::| ||| :::: ::|||||| |::||:||| ||||| |      :||: || |||||
Db          1 GDTAILRCVLEDKNSKVAWLNRSGIIFAGHDKWSLDPRVELEKRHSLEYSLRIQKVDVYD 60

Qy        110 EGPYTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTW 169
              || ||||||| : ||||:|:|||| ||| ||||:::|||:|::| |:| ||||| :||
Db         61 EGSYTCSVQTQHEPKTSQVYLIVQVPPKISNISSDVTVNEGSNVTLVCMANGRPEPVITW 120

Qy        170 RHISPKAVGFVSEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAK 229
              ||::|    |  |:|||| |||||||| ||| |:|:|::  |::|||||||| |:|:|
Db        121 RHLTPTGREFEGEEEYLEILGITREQSGKYECKAANEVSSADVKQVKVTVNYPPTITESK 180

Qy        230 GTGVPVGQKGTLQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHD 289
                  |:: :|:|||||||: :|:||:|| | |    |:::::    | |   ||:|
Db        181 SNEATTGRQASLKCEASAVPAPDFEWYRDDTR-INSANGLEIKSTEGQSSLTVTNVTEEH 239

Qy        290 YGNYTCVASNKLG 302
              ||||||||:||||
Db        240 YGNYTCVAANKLG 252
```

Search completed: September 11, 2003, 03:06:30
Job time : 36 secs

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;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  48:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  287 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-414-657D-48

  Query Match           49.1%;  Score 886.5;  DB 2;  Length 287;
  Best Local Similarity  56.6%;  Pred. No. 1.6e-80;
  Matches  164;  Conservative   57;  Mismatches   66;  Indels    3;  Gaps    2;

Qy         31 VRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTILYAGNDKWCLDPRVVL 90
              ||| |  | :  ||:||||::| ||| :::: ::|||||| |::||:||| ||||| |
Db          1 VRSVD--FNRGTDNITVRQGDTAILRCVLEDKNSKVAWLNRSGIIFAGHDKWSLDPRVEL 58

Qy         91 LSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEG 150
                 :||: || ||||||| ||||||| : ||||:|:||||| |||  ||||:::|||
Db         59 EKRHSLEYSLRIQKVDVYDEGSYTCSVQTQHEPKTSQVYLIVQVPPKISNISSDVTVNEG 118

Qy        151 NNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEIQGITREQSGDYECSASNDVAAP 210
              :|::| |:| ||||| :|||::|    |  |:||||| |||||||| ||| |:|:|::
Db        119 SNVTLVCMANGRPEPVITWRHLTPTGREFEGEEEYLEILGITREQSGKYECKAANEVSSA 178

Qy        211 VVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWYKDDKRLIEGKKGVK 270
               |::|||||||| |:|:|      |:: :|:|||||: :|:||:|| | |    |::
Db        179 DVKQVKVTVNYPPTITESKSNEATTGRQASLKCEASAVPAPDFEWYRDDTR-INSANGLE 237

Qy        271 VENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIMLFGPGAVSEVS 320
              :::    | |   ||:|  ||||||||:|||| ||||::|| ||:|  ::
Db        238 IKSTEGQSSLTVTNVTEEHYGNYTCVAANKLGVTNASLVLFRPGSVRGIN 287


RESULT 14
US-08-414-657D-49
; Sequence 49, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  49:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  287 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-414-657D-49

  Query Match           49.0%;  Score 885.5;  DB 2;  Length 287;
  Best Local Similarity  56.6%;  Pred. No. 2e-80;
  Matches  164;  Conservative   57;  Mismatches   66;  Indels    3;  Gaps    2;

Qy         31 VRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTILYAGNDKWCLDPRVVL 90
              ||| |  | :  ||:||||::| ||| :::: ::|||||| |::||:||| ||||| |
Db          1 VRSVD--FNRGTDNITVRQGDTAILRCVVEDKNSKVAWLNRSGIIFAGHDKWSLDPRVEL 58

Qy         91 LSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEG 150
                 :||: || ||||||| ||||||| : ||||:|:||||| |||  ||||:::|||
Db         59 EKRHALEYSLRIQKVDVYDEGSYTCSVQTQHEPKTSQVYLIVQVPPKISNISSDVTVNEG 118

Qy        151 NNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEIQGITREQSGDYECSASNDVAAP 210
              :|::| |:| ||||| :|||::|    |  |:||||| |||||||| ||| |:|:|::
Db        119 SNVTLVCMANGRPEPVITWRHLTPLGREFEGEEEYLEILGITREQSGKYECKAANEVSSA 178

Qy        211 VVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWYKDDKRLIEGKKGVK 270
               |::|||||||| |:|:|      |:: :|:|||||: :|:||:|| | |    |::
Db        179 DVKQVKVTVNYPPTITESKSNEATTGRQASLKCEASAVPAPDFEWYRDDTR-INSANGLE 237

Qy        271 VENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIMLFGPGAVSEVS 320
              :::    | |   ||:|  ||||||||:|||| ||||::|| ||:|  ::
Db        238 IKSTEGQSSLTVTNVTEEHYGNYTCVAANKLGVTNASLVLFRPGSVRGIN 287


RESULT 15
US-08-414-657D-56
; Sequence 56, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
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;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  45:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  310 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-414-657D-45

  Query Match             50.1%;  Score 905;  DB 2;  Length 310;
  Best Local Similarity   55.3%;  Pred. No. 2.5e-82;
  Matches  173;  Conservative   59;  Mismatches   77;  Indels    4;  Gaps    3;

Qy         31 VRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTILYAGNDKWCLDPRVVL 90
              ||| |  | :  ||:|||||::| ||| :::: ::|||||| |::||:||| ||||| |
Db          1 VRSVD--FNRGTDNITVRQGDTAILRCVVEDKNSKVAWLNRSGIIFAGHDKWSLDPRVEL 58

Qy         91 LSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEG 150
                 :||: || ||||||| ||||||| : ||||:|:||||| ||| ||||:::||| 
Db         59 EKRHALEYSLRIQKVDVYDEGSYTCSVQTQHEPKTSQVYLIVQVPPKISNISSDVTVNEG 118

Qy        151 NNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEIQGITREQSGDYECSASNDVAAP 210
              :|::| |:| ||||| :||||::|    |  |:|||| |||||||| ||| |:|:|::
Db        119 SNVTLVCMANGRPEPVITWRHLTPLGREFEGEEEYLEILGITREQSGKYECKAANEVSSA 178

Qy        211 VVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWYKDDKRLIEGKKGVK 270
               |::|||||||| |:|:|     |:: :|:|||||: :|:||:|| | |  |::
Db        179 DVKQVKVTVNYPPTITESKSNEATTGRQASLKCEASAVPAPDFEWYRDDTR-INSANGLE 237

Qy        271 VENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIMLFGPGAVSEVSNGTSRRAGCV 330
              :::    | |   ||:|  |||||||:|||| ||||::|| ||:|  : ||:   |  :
Db        238 IKSTEGQSSLTVTNVTEEHYGNYTCVAANKLGVTNASLVLFRPGSVRGI-NGSISLAVPL 296

Qy        331 WLLPLLVLHLLLK 343
              |||   :  || |
Db        297 WLLAASLFCLLSK 309


RESULT 12
US-08-414-657D-44
; Sequence 44, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  44:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  304 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-414-657D-44

  Query Match             49.9%;  Score 902;  DB 2;  Length 304;
  Best Local Similarity   55.5%;  Pred. No. 4.8e-82;
  Matches  171;  Conservative   59;  Mismatches   74;  Indels    4;  Gaps    3;

Qy         31 VRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTILYAGNDKWCLDPRVVL 90
              ||| |  | :: ||:|||||::| ||| :::: ::|||||| |::||:||| ||||| |
Db          1 VRSVD--FNRGTDNITVRQGDTAILRCVLEDKNSKVAWLNRSGIIFAGHDKWSLDPRVEL 58

Qy         91 LSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEG 150
                 :||: || ||||||| ||||||| : ||||:|:||||| ||| ||||:::||| 
Db         59 EKRHSLEYSLRIQKVDVYDEGSYTCSVQTQHEPKTSQVYLIVQVPPKISNISSDVTVNEG 118

Qy        151 NNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEIQGITREQSGDYECSASNDVAAP 210
              :|::| |:| ||||| :||||::|    |  |:|||| |||||||| ||| |:|:|::
Db        119 SNVTLVCMANGRPEPVITWRHLTPTGREFEGEEEYLEILGITREQSGKYECKAANEVSSA 178

Qy        211 VVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWYKDDKRLIEGKKGVK 270
              |::|||||||| |:|:|      |:: :|:|||||: :|:||:|| | |    |::
Db        179 DVKQVKVTVNYPPTITESKSNEATTGRQASLKCEASAVPAPDFEWYRDDTR-INSANGLE 237

Qy        271 VENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIMLFGPGAVSEVSNGTSRRAGCV 330
              :::    | |.  ||:|  |||||||:|||| ||||::|| ||:|  : ||:   |  :
Db        238 IKSTEGQSSLTVTNVTEEHYGNYTCVAANKLGVTNASLVLFRPGSVRGI-NGSISLAVPL 296

Qy        331 WLLPLLVL 338
              |||   :|
Db        297 WLLAASLL 304


RESULT 13
US-08-414-657D-48
; Sequence 48, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
```

```
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ for Windows Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/414,657D
;       FILING DATE:  31-MAR-1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Bloom, Allen
;       REGISTRATION NUMBER:  29,135
;       REFERENCE/DOCKET NUMBER:  317743-102
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  609-520-3214
;       TELEFAX:  609-520-3259
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  46:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  308 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-414-657D-46

  Query Match           50.3%;  Score 908;  DB 2;  Length 308;
  Best Local Similarity   56.3%;  Pred. No. 1.2e-82;
  Matches  170;  Conservative   58;  Mismatches   70;  Indels    4;  Gaps    3;

Qy         20 LAALCLF-QGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTILYAG 78
              |  |||   |:|||| |  | :  ||:|||||::| ||| :::: ::|||||| |::||
Db         10 LRLLCLLPTGLPVRSVD--FNRGTDNITVRQGDTAILRCVLEDKNSKVAWLNRSGIIPAG 67

Qy         79 NDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKI 138
              :||| ||||| |      :||: || ||||||| ||||||| : ||||:|:|||| |||
Db         68 HDKWSLDPRVELEKRHSLEYSLRIQKVDVYDEGSYTCSVQTQHEPKTSQVYLIVQVPPKI 127

Qy        139 VEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEIQGITREQSGD 198
              ||||:::|||:|::| |:| ||||| :||||::|    |  |:||||| ||||||||
Db        128 SNISSDVTVNEGSNVTLVCMANGRPEPVITWRHLTPTGREFEGEEEYLEILGITREQSGK 187

Qy        199 YECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWYKD 258
              ||| |:|:|::  |::|||||||||| |:|:|      |:: :|:|||||||: :|:||:|
Db        188 YECKAANEVSSADVKQVKVTVNYPPTITESKSNEATTGRQASLKCEASAVPAPDFEWYRD 247

Qy        259 DKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIMLFGPGAVSE 318
              | | |    |:::::   :| |   ||:|  |||||||:|||| ||||::|| ||:|
Db        248 DTR-INSANGLEIKSTEGQSSLTVTNVTEEHYGNYTCVAANKLGVTNASLVLFRPGSVRG 306

Qy        319 VS 320
              ::
Db        307 IN 308


RESULT 10
US-08-414-657D-47
; Sequence 47, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  47:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  315 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-414-657D-47

  Query Match           50.2%;  Score 907;  DB 2;  Length 315;
  Best Local Similarity   56.3%;  Pred. No. 1.6e-82;
  Matches  170;  Conservative   58;  Mismatches   70;  Indels    4;  Gaps    3;

Qy         20 LAALCLF-QGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTILYAG 78
              |  |||   |:|||| |  | :  ||:|||||::| ||| :::: ::|||||| |::||
Db         17 LRLLCLLPTGLPVRSVD--FNRGTDNITVRQGDTAILRCVVEDKNSKVAWLNRSGIIPAG 74

Qy         79 NDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKI 138
              :||| ||||| |      :||: || ||||||| ||||||| : ||||:|:|||| |||
Db         75 HDKWSLDPRVELEKRHALEYSLRIQKVDVYDEGSYTCSVQTQHEPKTSQVYLIVQVPPKI 134

Qy        139 VEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEIQGITREQSGD 198
              ||||:::|||:|::| |:| ||||| :||||::|    |  |:||||| ||||||||
Db        135 SNISSDVTVNEGSNVTLVCMANGRPEPVITWRHLTPLGREFEGEEEYLEILGITREQSGK 194

Qy        199 YECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWYKD 258
              ||| |:|:|::  |::|||||||||| |:|:|      |:: :|:|||||||: :|:||:|
Db        195 YECKAANEVSSADVKQVKVTVNYPPTITESKSNEATTGRQASLKCEASAVPAPDFEWYRD 254

Qy        259 DKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIMLFGPGAVSE 318
              | | |    |:::::   :| |   ||:|  |||||||:|||| ||||::|| ||:|
Db        255 DTR-INSANGLEIKSTEGQSSLTVTNVTEEHYGNYTCVAANKLGVTNASLVLFRPGSVRG 313

Qy        319 VS 320
              ::
Db        314 IN 315


RESULT 11
US-08-414-657D-45
; Sequence 45, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
```

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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  60:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  338 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-414-657D-60

  Query Match           51.1%;  Score 923.5;  DB 2;  Length 338;
  Best Local Similarity  55.1%;  Pred. No. 4e-84;
  Matches  179;  Conservative   60;  Mismatches   81;  Indels    5;  Gaps    4;

Qy         20 LAALCLF-QGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTILYAG 78
              |  |||   |:|||| |  | :  ||:||||||::| ||| :::: ::|||||||| |::||
Db         17 LRLLCLLPTGLPVRSVD--FNRGTDNITVRQGDTAILRCVLEDKNSKVAWLNRSGIIFAG 74

Qy         79 NDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKI 138
              :||| ||||| |      :||: || ||||||| ||||||| : ||||:|:||||| |||
Db         75 HDKWSLDPRVELEKRHSLEYSLRIQKVDVYDEGSYTCSVQTQHEPKTSQVYLIVQVPPKI 134

Qy        139 VEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEIQGITREQSGD 198
               ||||:::|||:|::| |:| ||||| :||||::|    |  |:||||| ||||||||
Db        135 SNISSDVTVNEGSNVTLVCMANGRPEPVITWRHLTPTGREFEGEEEYLEILGITREQSGK 194

Qy        199 YECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWYKD 258
              ||| |:|:|::  |::|||||||||| |:|:|      |:: :|:|||||||: :|:|||:|
Db        195 YECKAANEVSSADVKQVKVTVNYPPTITESKSNEATTGRQASLKCEASAVPAPDFEWYRD 254

Qy        259 DKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIMLFGPGAVSE 318
              | | |    |:::::    | |    |:|  ||||||||:|||| ||||::|| ||:|
Db        255 DTR-INSANGLEIKSTEGQSSLTVTMVTEEHYGNYTCVAANKLGVTNASLVLFRPGSVRG 313

Qy        319 VSNGTSRRAGCVWLLPLLVLHLLLK 343
              : ||:   |  :|||   :| || |
Db        314 I-NGSISLAVPLWLLAASLLCLLSK 337


RESULT 8
US-09-135-080-8
; Sequence 8, Application US/09135080
; Patent No. 6423827
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat R.
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/135,080
;      FILING DATE:  17-AUG-1998
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/414,657
;      FILING DATE:  31-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-620-3214
;      TELEFAX:  609-620-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  338 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-135-080-8

  Query Match           51.1%;  Score 923.5;  DB 4;  Length 338;
  Best Local Similarity  55.1%;  Pred. No. 4e-84;
  Matches  179;  Conservative   60;  Mismatches   81;  Indels    5;  Gaps    4;

Qy         20 LAALCLF-QGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTILYAG 78
              |  |||   |:|||| |  | :  ||:||||||::| ||| :::: ::|||||||| |::||
Db         17 LRLLCLLPTGLPVRSVD--FNRGTDNITVRQGDTAILRCVLEDKNSKVAWLNRSGIIFAG 74

Qy         79 NDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKI 138
              :||| ||||| |      :||: || ||||||| ||||||| : ||||:|:||||| |||
Db         75 HDKWSLDPRVELEKRHSLEYSLRIQKVDVYDEGSYTCSVQTQHEPKTSQVYLIVQVPPKI 134

Qy        139 VEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEIQGITREQSGD 198
               ||||:::|||:|::| |:| ||||| :||||::|    |  |:||||| ||||||||
Db        135 SNISSDVTVNEGSNVTLVCMANGRPEPVITWRHLTPTGREFEGEEEYLEILGITREQSGK 194

Qy        199 YECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWYKD 258
              ||| |:|:|::  |::|||||||||| |:|:|      |:: :|:|||||||: :|:|||:|
Db        195 YECKAANEVSSADVKQVKVTVNYPPTITESKSNEATTGRQASLKCEASAVPAPDFEWYRD 254

Qy        259 DKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIMLFGPGAVSE 318
              | | |    |:::::    | |    |:|  ||||||||:|||| ||||::|| ||:|
Db        255 DTR-INSANGLEIKSTEGQSSLTVTMVTEEHYGNYTCVAANKLGVTNASLVLFRPGSVRG 313

Qy        319 VSNGTSRRAGCVWLLPLLVLHLLLK 343
              : ||:   |  :|||   :| || |
Db        314 I-NGSISLAVPLWLLAASLLCLLSK 337


RESULT 9
US-08-414-657D-46
; Sequence 46, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
```

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;       TELEPHONE:  609-520-3214
;       TELEFAX:  609-520-3259
;       TELEX:
;  INFORMATION FOR SEQ ID NO:  41:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH:  325 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-414-657D-41

  Query Match             51.1%;  Score 923.5;  DB 2;  Length 325;
  Best Local Similarity   55.3%;  Pred. No. 3.8e-84;
  Matches  177;  Conservative   60;  Mismatches   78;  Indels    5;  Gaps    4;

Qy         20 LAALCLF-QGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTILYAG 78
              |  |||   |:|||| |  | :  ||:|||||::| ||| :::: ::|||||||  |::||
Db         10 LRLLCLLPTGLPVRSVD--FNRGTDNITVRQGDTAILRCVLEDKNSKVAWLNRSGIIFAG 67

Qy         79 NDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKI 138
              :||| ||||| |      :|| ||||||| ||||||| : ||||:|:||||| |||
Db         68 HDKWSLDPRVELEKRHSLEYSLRIQKVDVYDEGSYTCSVQTQHEPKTSQVYLIVQVPPKI 127

Qy        139 VEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEIQGITREQSGD 198
              ||||:::|||:|::| |:| ||||| :||||::|    |  |:||||| ||||||||
Db        128 SNISSDVTVNEGSNVTLVCMANGRPEPVITWRHLTPTGREFEGEEEYLEILGITREQSGK 187

Qy        199 YECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWYKD 258
              ||| |:|:|::  |::|||||||| |:|:|      |:: :|:|||||||: :|:||:|
Db        188 YECKAANEVSSADVKQVKVTVNYPPTITESKSNEATTGRQASLKCEASAVPAPDFEWYRD 247

Qy        259 DKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIMLFGPGAVSE 318
              | | |    |:::::    | |   ||:|  ||||||||:|||| ||||::|| ||:|
Db        248 DTR-INSANGLEIKSTEGQSSLTVTNVTEEHYGNYTCVAANKLGVTNASLVLFRPGSVRG 306

Qy        319 VSNGTSRRAGCVWLLPLLVL 338
              : ||:   |  :|||  :|
Db        307 I-NGSISLAVPLWLLAASLL 325


RESULT 6
US-09-135-080-2
; Sequence 2, Application US/09135080
; Patent No. 6423827
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat R.
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/135,080
;      FILING DATE:  17-AUG-1998
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/414,657
;      FILING DATE:  31-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-620-3214
;      TELEFAX:  609-620-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  325 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-09-135-080-2

  Query Match             51.1%;  Score 923.5;  DB 4;  Length 325;
  Best Local Similarity   55.3%;  Pred. No. 3.8e-84;
  Matches  177;  Conservative   60;  Mismatches   78;  Indels    5;  Gaps    4;

Qy         20 LAALCLF-QGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTILYAG 78
              |  |||   |:|||| |  | :  ||:|||||::| ||| :::: ::|||||||  |::||
Db         10 LRLLCLLPTGLPVRSVD--FNRGTDNITVRQGDTAILRCVLEDKNSKVAWLNRSGIIFAG 67

Qy         79 NDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKI 138
              :||| ||||| |      :|| ||||||| ||||||| : ||||:|:||||| |||
Db         68 HDKWSLDPRVELEKRHSLEYSLRIQKVDVYDEGSYTCSVQTQHEPKTSQVYLIVQVPPKI 127

Qy        139 VEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEIQGITREQSGD 198
              ||||:::|||:|::| |:| ||||| :||||::|    |  |:||||| ||||||||
Db        128 SNISSDVTVNEGSNVTLVCMANGRPEPVITWRHLTPTGREFEGEEEYLEILGITREQSGK 187

Qy        199 YECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWYKD 258
              ||| |:|:|::  |::|||||||| |:|:|      |:: :|:|||||||: :|:||:|
Db        188 YECKAANEVSSADVKQVKVTVNYPPTITESKSNEATTGRQASLKCEASAVPAPDFEWYRD 247

Qy        259 DKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIMLFGPGAVSE 318
              | | |    |:::::    | |   ||:|  ||||||||:|||| ||||::|| ||:|
Db        248 DTR-INSANGLEIKSTEGQSSLTVTNVTEEHYGNYTCVAANKLGVTNASLVLFRPGSVRG 306

Qy        319 VSNGTSRRAGCVWLLPLLVL 338
              : ||:   |  :|||  :|
Db        307 I-NGSISLAVPLWLLAASLL 325


RESULT 7
US-08-414-657D-60
; Sequence 60, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
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;      TOPOLOGY:  linear
US-09-135-080-4

  Query Match           51.3%;  Score 926.5;  DB 4;  Length 338;
  Best Local Similarity   55.1%;  Pred. No. 2e-84;
  Matches  179;  Conservative   60;  Mismatches   81;  Indels    5;  Gaps    4;

Qy         20 LAALCLF-QGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTILYAG 78
              |  |||   |:|||| |  | :  ||:||||||:| ||| :::: ::|||||| |::||
Db         17 LRLLCLLPTGLPVRSVD--FNRGTDNITVRQGDTAILRCVVEDKNSKVAWLNRSGIIFAG 74

Qy         79 NDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKI 138
              :||| ||||| |      :||: || ||||||| ||||||| : ||||:|:||||| |||
Db         75 HDKWSLDPRVELEKRHALEYSLRIQKVDVYDEGSYTCSVQTQHEPKTSQVYLIVQVPPKI 134

Qy        139 VEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEIQGITREQSGD 198
              |||:::|||:|::| |:| ||||| :||||::|    |  |:||||| ||||||||
Db        135 SNISSDVTVNEGSNVTLVCMANGRPEPVITWRHLTPLGREFEGEEEYLEILGITREQSGK 194

Qy        199 YECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWYKD 258
              ||| |:|:|::  |::|||||||| |:|:|      |:: :|:|||||||: :|:||:|
Db        195 YECKAANEVSSADVKQVKVTVNYPPTITESKSNEATTGRQASLKCEASAVPAPDFEWYRD 254

Qy        259 DKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIMLFGPGAVSE 318
              | | |.   |:::::    | |   ||:|  |||||||:|||| ||||::|| ||:|
Db        255 DTR-INSANGLEIKSTEGQSSLTVTNVTEEHYGNYTCVAANKLGVTNASLVLFRPGSVRG 313

Qy        319 VSNGTSRRAGCVWLLPLLVLHLLLK 343
              : ||:   |  :|||   :  || |
Db        314 I-NGSISLAVPLWLLAASLFCLLSK 337


RESULT 4
US-08-414-657D-2
; Sequence 2, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
;   APPLICANT:  Levitt, Pat
;   APPLICANT:  Pimenta, Aurea
;   APPLICANT:  Fischer, Itzhak
;   APPLICANT:  Zhukareva, Victoria
;   TITLE OF INVENTION:  Limbic System-Associated Membrane
;   TITLE OF INVENTION:  Protein and DNA
;   NUMBER OF SEQUENCES:  60
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Dechert Price & Rhoads
;     STREET:  997 Lenox Drive, Building 3, Suite 210
;     CITY:  Lawrenceville
;     STATE:  NJ
;     COUNTRY:  USA
;     ZIP:  08543
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Diskette
;     COMPUTER:  IBM Compatible
;     OPERATING SYSTEM:  DOS
;     SOFTWARE:  FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/414,657D
;     FILING DATE:  31-MAR-1995
;     CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Bloom, Allen
;     REGISTRATION NUMBER:  29,135
;     REFERENCE/DOCKET NUMBER:  317743-102
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  609-520-3214
;     TELEFAX:  609-520-3259
;     TELEX:
; INFORMATION FOR SEQ ID NO:  2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  325 amino acids
;     TYPE:  amino acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
;   FRAGMENT TYPE:  internal
US-08-414-657D-2

  Query Match           51.1%;  Score 923.5;  DB 2;  Length 325;
  Best Local Similarity   55.3%;  Pred. No. 3.8e-84;
  Matches  177;  Conservative   60;  Mismatches   78;  Indels    5;  Gaps    4;

Qy         20 LAALCLF-QGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTILYAG 78
              |  |||   |:|||| |  | :  ||:||||||:| ||| :::: ::|||||| |::||
Db         10 LRLLCLLPTGLPVRSVD--FNRGTDNITVRQGDTAILRCVLEDKNSKVAWLNRSGIIFAG 67

Qy         79 NDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKI 138
              :||| ||||| |      :||: || ||||||| ||||||| : ||||:|:||||| |||
Db         68 HDKWSLDPRVELEKRHSLEYSLRIQKVDVYDEGSYTCSVQTQHEPKTSQVYLIVQVPPKI 127

Qy        139 VEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEIQGITREQSGD 198
              |||:::|||:|::| |:| ||||| :||||::|    |  |:||||| ||||||||
Db        128 SNISSDVTVNEGSNVTLVCMANGRPEPVITWRHLTPTGREFEGEEEYLEILGITREQSGK 187

Qy        199 YECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWYKD 258
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Db        188 YECKAANEVSSADVKQVKVTVNYPPTITESKSNEATTGRQASLKCEASAVPAPDFEWYRD 247

Qy        259 DKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIMLFGPGAVSE 318
              | | |.   |:::::    | |   ||:|  |||||||:|||| ||||::|| ||:|
Db        248 DTR-INSANGLEIKSTEGQSSLTVTNVTEEHYGNYTCVAANKLGVTNASLVLFRPGSVRG 306

Qy        319 VSNGTSRRAGCVWLLPLLVL 338
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Db        307 I-NGSISLAVPLWLLAASLL 325


RESULT 5
US-08-414-657D-41
; Sequence 41, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
;   APPLICANT:  Levitt, Pat
;   APPLICANT:  Pimenta, Aurea
;   APPLICANT:  Fischer, Itzhak
;   APPLICANT:  Zhukareva, Victoria
;   TITLE OF INVENTION:  Limbic System-Associated Membrane
;   TITLE OF INVENTION:  Protein and DNA
;   NUMBER OF SEQUENCES:  60
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Dechert Price & Rhoads
;     STREET:  997 Lenox Drive, Building 3, Suite 210
;     CITY:  Lawrenceville
;     STATE:  NJ
;     COUNTRY:  USA
;     ZIP:  08543
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Diskette
;     COMPUTER:  IBM Compatible
;     OPERATING SYSTEM:  DOS
;     SOFTWARE:  FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/414,657D
;     FILING DATE:  31-MAR-1995
;     CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Bloom, Allen
;     REGISTRATION NUMBER:  29,135
;     REFERENCE/DOCKET NUMBER:  317743-102
;   TELECOMMUNICATION INFORMATION:
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Qy         20 LAALCLF-QGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTILYAG 78
              |  |||   |:|||| |  | :  ||:||||||:| ||| :::: ::|||||||| |::||
Db         17 LRLLCLLPTGLPVRSVD--FNRGTDNITVRQGDTAILRCVVEDKNSKVAWLNRSGIIFAG 74

Qy         79 NDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKI 138
              :||| ||||| |      :||: || ||||||| ||||||| : ||||:|:||||| |||
Db         75 HDKWSLDPRVELEKRHALEYSLRIQKVDVYDEGSYTCSVQTQHEPKTSQVYLIVQVPPKI 134

Qy        139 VEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEIQGITREQSGD 198
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Db        135 SNISSDVTVNEGSNVTLVCMANGRPEPVITWRHLTPLGREFEGEEEYLEILGITREQSGK 194

Qy        199 YECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWYKD 258
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Db        195 YECKAANEVSSADVKQVKVTVNYPPTITESKSNEATTGRQASLKCEASAVPAPDFEWYRD 254

Qy        259 DKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIMLFGPGAVSE 318
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Qy        319 VSNGTSRRAGCVWLLPLLVLHLLLK 343
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Db        314 I-NGSISLAVPLWLLAASLFCLLSK 337


RESULT 2
US-08-414-657D-43
; Sequence 43, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  43:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  338 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-414-657D-43
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  Query Match           51.3%;  Score 926.5;  DB 2;  Length 338;
  Best Local Similarity  55.1%;  Pred. No. 2e-84;
  Matches  179;  Conservative   60;  Mismatches   81;  Indels    5;  Gaps    4;

Qy         20 LAALCLF-QGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTILYAG 78
              |  |||   |:|||| |  | :  ||:||||||:| ||| :::: ::|||||||| |::||
Db         17 LRLLCLLPTGLPVRSVD--FNRGTDNITVRQGDTAILRCVVEDKNSKVAWLNRSGIIFAG 74

Qy         79 NDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKI 138
              :||| ||||| |      :||: || ||||||| ||||||| : ||||:|:||||| |||
Db         75 HDKWSLDPRVELEKRHALEYSLRIQKVDVYDEGSYTCSVQTQHEPKTSQVYLIVQVPPKI 134

Qy        139 VEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEIQGITREQSGD 198
               ||||:::|||:|::| |:| ||||| :||||::|    |  |:||||| ||||||||
Db        135 SNISSDVTVNEGSNVTLVCMANGRPEPVITWRHLTPLGREFEGEEEYLEILGITREQSGK 194

Qy        199 YECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWYKD 258
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Db        195 YECKAANEVSSADVKQVKVTVNYPPTITESKSNEATTGRQASLKCEASAVPAPDFEWYRD 254

Qy        259 DKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIMLFGPGAVSE 318
              | | |    |:::::    | |   ||:|  |||||||:|||| ||||::|| ||:|
Db        255 DTR-INSANGLEIKSTEGQSSLTVTNVTEEHYGNYTCVAANKLGVTNASLVLFRPGSVRG 313

Qy        319 VSNGTSRRAGCVWLLPLLVLHLLLK 343
              : ||:   |  :|||   :  || |
Db        314 I-NGSISLAVPLWLLAASLFCLLSK 337


RESULT 3
US-09-135-080-4
; Sequence 4, Application US/09135080
; Patent No. 6423827
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat R.
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/135,080
;      FILING DATE:  17-AUG-1998
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/414,657
;      FILING DATE:  31-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-620-3214
;      TELEFAX:  609-620-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  338 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 11, 2003, 03:03:33 ; Search time 35 Seconds
(without alignments)
415.855 Million cell updates/sec

Title: US-10-017-084A-523
Perfect score: 1806
Sequence: 1 MKTIQPKMHNSISWAIFTGL.....RRAGCVWLLPLLVLHLLLKF 344

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	926.5	51.3	338	2	US-08-414-657D-42	Sequence 42, Appl
2	926.5	51.3	338	2	US-08-414-657D-43	Sequence 43, Appl
3	926.5	51.3	338	4	US-09-135-080-4	Sequence 4, Appli
4	923.5	51.1	325	2	US-08-414-657D-2	Sequence 2, Appli
5	923.5	51.1	325	2	US-08-414-657D-41	Sequence 41, Appl
6	923.5	51.1	325	4	US-09-135-080-2	Sequence 2, Appli
7	923.5	51.1	338	2	US-08-414-657D-60	Sequence 60, Appl
8	923.5	51.1	338	4	US-09-135-080-8	Sequence 8, Appli
9	908	50.3	308	2	US-08-414-657D-46	Sequence 46, Appl
10	907	50.2	315	2	US-08-414-657D-47	Sequence 47, Appl
11	905	50.1	310	2	US-08-414-657D-45	Sequence 45, Appl
12	902	49.9	304	2	US-08-414-657D-44	Sequence 44, Appl
13	886.5	49.1	287	2	US-08-414-657D-48	Sequence 48, Appl
14	885.5	49.0	287	2	US-08-414-657D-49	Sequence 49, Appl
15	796.5	44.1	252	2	US-08-414-657D-56	Sequence 56, Appl
16	795.5	44.0	252	2	US-08-414-657D-57	Sequence 57, Appl
17	261	14.5	1395	3	US-09-540-245A-15	Sequence 15, Appl
18	256	14.2	421	2	US-08-659-984A-1	Sequence 1, Appli
19	256	14.2	421	3	US-08-660-531-1	Sequence 1, Appli
20	256	14.2	444	2	US-08-659-984A-5	Sequence 5, Appli
21	256	14.2	444	3	US-08-660-531-5	Sequence 5, Appli
22	249.5	13.8	607	2	US-08-752-307B-12	Sequence 12, Appl
23	249.5	13.8	607	4	US-09-707-802-12	Sequence 12, Appl
24	249.5	13.8	607	4	US-09-991-326-12	Sequence 12, Appl
25	246.5	13.6	1018	1	US-08-408-093-6	Sequence 6, Appli
26	246.5	13.6	1018	1	US-08-408-420A-6	Sequence 6, Appli
27	246.5	13.6	1018	1	US-08-714-901-6	Sequence 6, Appli
28	246.5	13.6	1018	3	US-08-040-741-6	Sequence 6, Appli
29	243.5	13.5	605	2	US-08-752-307B-8	Sequence 8, Appli
30	243.5	13.5	605	4	US-09-707-802-8	Sequence 8, Appli
31	243.5	13.5	605	4	US-09-991-326-8	Sequence 8, Appli
32	243.5	13.5	1018	1	US-08-452-052-2	Sequence 2, Appli
33	237	13.1	73	2	US-08-414-657D-50	Sequence 50, Appl
34	237	13.1	73	2	US-08-414-657D-51	Sequence 51, Appl
35	230.5	12.8	868	1	US-08-374-834-1	Sequence 1, Appli
36	230.5	12.8	868	2	US-08-644-271-1	Sequence 1, Appli
37	230.5	12.8	868	4	US-09-077-955-1	Sequence 1, Appli
38	229.5	12.7	869	1	US-08-374-834-16	Sequence 16, Appl
39	229.5	12.7	869	2	US-08-644-271-29	Sequence 29, Appl
40	229.5	12.7	869	4	US-09-077-955-33	Sequence 33, Appl
41	225.5	12.5	478	5	PCT-US95-08493-15	Sequence 15, Appl
42	225.5	12.5	860	5	PCT-US95-08493-19	Sequence 19, Appl
43	225.5	12.5	868	5	PCT-US95-08493-21	Sequence 21, Appl
44	220.5	12.2	423	4	US-09-778-510-22	Sequence 22, Appl
45	220.5	12.2	442	4	US-09-778-510-20	Sequence 20, Appl

ALIGNMENTS

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RESULT 1
US-08-414-657D-42
; Sequence 42, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  42:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  338 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-414-657D-42

  Query Match           51.3%;  Score 926.5;  DB 2;  Length 338;
  Best Local Similarity  55.1%;  Pred. No. 2e-84;
  Matches  179;  Conservative   60;  Mismatches   81;  Indels    5;  Gaps    4;
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RL   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99264333; PubMed=10330412;
RA   Marg A., Sirim P., Spaltmann F., Plagge A., Kauselmann G., Buck F.,
RA   Rathjen F.G., Brummendorf T.;
RT   "Neurotractin, A novel neurite outgrowth-promoting Ig-like protein
RT   that interacts with CEPU-1 and LAMP.";
RL   J. Cell Biol. 145:865-876(1999).
DR   EMBL; AJ132998; CAB44445.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain.
SQ   SEQUENCE   261 AA;  28205 MW;  80E74DFA658802F3 CRC64;

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  Best Local Similarity   52.6%;  Pred. No. 1.2e-42;
  Matches  112;  Conservative   45;  Mismatches   54;  Indels    2;  Gaps    2;

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              |||:|::||:||| :|||| : :   : :||::||:||| |:|||||||| : |:| :||
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Qy        190 GITREQSGDYECSASNDVAAPVVRRVKVTVNYP 222
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AC   Q8N440;
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DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RA   Strausberg R.;
RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC036771; AAH36771.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00408; IGc2; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Hypothetical protein; Immunoglobulin domain.
SQ   SEQUENCE   226 AA;  24733 MW;  61EBC9E93977B520 CRC64;

  Query Match           30.2%;  Score 545.5;  DB 4;  Length 226;
  Best Local Similarity   49.3%;  Pred. No. 3.2e-38;
  Matches  103;  Conservative   40;  Mismatches   65;  Indels    1;  Gaps    1;

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              :||| ||| |||::||:|:::||| |::|||:|||:|||:::|||||| |   |     :||
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              ||   |:||| :|:|  |::|: ::|    | |   ||::  :|||||||:|||| |||
Db        121 GVPPPAFEWYKGEKKLFNGQQGIIIQNFSTRSILTVTNVTQEHFGNYTCVAANKLGTTNA 180

Qy        307 SIMLFGPGAVSEVSNGTSRRAGCVWLLPL 335
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Search completed: September 11, 2003, 03:04:57
Job time : 82 secs
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              |||:|::|| ||| :|||| : :  :  ||::|||||| |:|||||||| : |:| :||
Db         73 NRSSIIFAGGDKWSVDPRVSISTLNKRDYSLQIQNVDVTDDGPYTCSVQTQHTPRTMQVH 132

Qy        130 LIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEIQ 189
              | ||| ||| :||:|:::||| |::|||:|||:||| ::|||||| |  |    :||:|
Db        133 LTVQVPPKIYDISNDMTVNEGTNVTLTCLATGKPEPFISWRHISPSAKPF-ENGQYLDIY 191

Qy        190 GITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVP 249
              ||||:|:|:||||| |||: | ||:||| ||:.| | | |    |  |: | ::||. : ||
Db        192 GITRDQAGEYECSAENDVSFPDVRKVKVVVNFAPTIQEIKSGTVTPGRSGLIRCEGAGVP 251

Qy        250 SAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIM 309
                |:||| :|:|  |::|: ::|    | |  :||::  :|||||||:|||| ||||:
Db        252 PPAFEWYKGEKKLFNGQQGIIIQNFSTRSILTVTNVTQEHFGNYTCVAANKLGTTNASLP 311

Qy        310 LFGPGAVSEVSNGTSRRAGCVWLLPL 335
              |  |          |::      | | |
Db        312 LNPPSTAQYGITGSADVLFSCWYLVL 337


RESULT 12
Q8HW98
ID   Q8HW98      PRELIMINARY;      PRT;   325 AA.
AC   Q8HW98;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Adult male hypothalamus cDNA, RIKEN full-length enriched library,
DE   clone:A230106M20 product:weakly similar to limbic system-associated
DE   membrane protein precursor (E19S) (CHLAMP, G19-isoform)
DE   (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK039193; BAC30273.1; -.
FT   NON_TER       1       1
SQ   SEQUENCE   325 AA;  35609 MW;  F4277BA4A416F707 CRC64;

  Query Match           42.0%;  Score 759;  DB 7;  Length 325;
  Best Local Similarity  50.3%;  Pred. No. 4.4e-56;
  Matches  163;  Conservative   45;  Mismatches  104;  Indels   12;  Gaps    6;

Qy         15 AIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTI 74
              |   ||| :   :|  : |    |    || || :|::||| | ||  |||||||||| |
Db          5 AALAGLAVIS--RG--LLSQSLEFSSPADNYTVCEGDNATLSCFIDEHVTRVAWLNRSNI 60

Qy         75 LYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQV 134
              ||||||:|  |||| || ||  :|| |  | : ||| |||| || : | |::|:||| |
Db         61 LYAGNDRWTSDPRVRLLINTPEEFSILITQVGLGDEGLYTCSFQTRHQPYTTQVYLIVHV 120

Qy        135 SPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEIQGITRE 194
              :|| ||| :::||| |::| |:|  ||||||||| :    || || | |||  | |
Db        121 PARIVNISSPVAVNEGGNVNLLCLAVGRPEPTVTWRQLRD---GFTSEGEILEISDIQRG 177

Qy        195 QSGDYECSASNDV-AAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEF 253
              |:|:|||   :| | :||  ||| ||||||| |::       :|:   |:||| ||| |:|
Db        178 QAGEYECVTHDGVNSAPDSRRVLVTVNYPPTITDVTSARTALGRAALLRCEAMAVPPADF 237

Qy        254 QWYKDDKRLIEGK-KGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIMLFG 312
              ||||||: | :|  :|:|||:     | |:| |||   |||||| |:|:|| ::||: |
Db        238 QWYKDDRLLSSGSAEGLKVQTERTRSMLLFANVSARHYGNYTCRAANRLGASSASMRLLR 297

Qy        313 PGAVSEVSNGTSRRAGCVWLLPLL 336
              ||:   : |  |  | : ||  |
Db        298 PGS---LENSAPRPPGPLTLLSAL 318


RESULT 13
Q8BMT5
ID   Q8BMT5      PRELIMINARY;      PRT;   188 AA.
AC   Q8BMT5;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Weakly similar to opioid binding protein/cell adhesion molecule
DE   precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Embryo;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK028345; BAC25895.1; -.
SQ   SEQUENCE   188 AA;  20937 MW;  F19534D6F78489DC CRC64;

  Query Match           38.0%;  Score 686.5;  DB 11;  Length 188;
  Best Local Similarity  74.1%;  Pred. No. 2.8e-50;
  Matches  129;  Conservative   18;  Mismatches   24;  Indels    3;  Gaps    1;

Qy         12 ISWAIFTGLAALCLF---QGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAW 68
              : |     ::   ||   |||||||||||||||||||||||||||||||:|||||||
Db          9 LPWKCLVVVSLRLLFLVPTGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDDRVTRVAW 68

Qy         69 LNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRV 128
              |||||||||||||| :|||||:| || |||||  ||||||||||||||||||||||||||
Db         69 LNRSTILYAGNDKWSIDPRVIILVNTPTQYSIMIQNVDVYDEGPYTCSVQTDNHPKTSRV 128

Qy        129 HLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSE 182
              |||||| |:|: ||||||:|||:::::| |:| ||||||||||:| |    |  :
Db        129 HLIVQVPPQIMNISSDITVNEGSSVTLLCLAIGRPEPTVTWRHLSVKGKVFTMQ 182


RESULT 14
Q9W6V1
ID   Q9W6V1      PRELIMINARY;      PRT;   261 AA.
AC   Q9W6V1;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Neurotractin-S.
GN   NTRA-S.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bruemmendorf T.;
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DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Limbic system-associated membrane protein precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK044845; BAC32117.1; -.
SQ   SEQUENCE   341 AA;  38086 MW;  949CE792C67E25C3 CRC64;

  Query Match           49.5%;  Score 894;  DB 11;  Length 341;
  Best Local Similarity  56.3%;  Pred. No. 1.7e-67;
  Matches  169;  Conservative   56;  Mismatches   71;  Indels   4;  Gaps    3;

Qy         20 LAALCLF-QGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTILYAG 78
              |  |||   |:|||| |  | :  ||:||||:::| ||| :::: ::|||||||  |:::|
Db         17 LRLLCLLPTGLPVRSVD--FNRGTDNITVRQGDTAILRCVVEDKNSKVAWLNRSGIIFAG 74

Qy         79 NDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKI 138
              :||| ||||| |      :||: || ||||||| ||||||| : ||||:|:|||||| |||
Db         75 HDKWSLDPRVELEKRHALEYSLRIQKVDVYDEGSYTCSVQTQHEPKTSQVYLIVQVPPKI 134

Qy        139 VEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEIQGITREQSGD 198
               ||||:::|||:|:::| |:| ||||| :||||::|    |  |:|||||| ||||||||
Db        135 SNISSDVTVNEGSNVTLVCMANGRPEPVITWRHLTPLGREFEGEEEYLEILGITREQSGK 194

Qy        199 YECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWYKD 258
              ||| |:|:|::  |::|||||||||| |:|:|      |:: :|:|||||||: :|:||:|
Db        195 YECKAANEVSSADVKQVKVTVNYPPTITESKSNEATTGRQASLKCEASAVPAPDFEWYRD 254

Qy        259 DKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIMLFGPGAVSE 318
              | | |   |:::::    | |   ||:|  ||||||||:|||| ||||::||   | :|
Db        255 DTR-INSANGLEIKSTEGQSSLTVTNVTEEHYGNYTCVAANKLGVTNASLVLFSKYAKTE 313


RESULT 10
Q9W6V2
ID   Q9W6V2      PRELIMINARY;      PRT;  352 AA.
AC   Q9W6V2;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Neurotractin-L.
GN   NTRA-L.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Bruemmendorf T.;
RL   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=99264333; PubMed=10330412;
RA   Marg A., Sirim P., Spaltmann F., Plagge A., Kauselmann G., Buck F.,
RA   Rathjen F.G., Brummendorf T.;
RT   "Neurotractin, A novel neurite outgrowth-promoting Ig-like protein
RT   that interacts with CEPU-1 and LAMP.";
RL   J. Cell Biol. 145:865-876(1999).
DR   EMBL; AJ132999; CAB44446.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00408; IGc2; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
KW   Immunoglobulin domain.
SQ   SEQUENCE   352 AA;  37944 MW;  B0FA99F295FD8FA0 CRC64;

  Query Match           46.6%;  Score 842;  DB 13;  Length 352;
  Best Local Similarity  48.0%;  Pred. No. 4.6e-63;
  Matches  159;  Conservative   68;  Mismatches  102;  Indels   2;  Gaps    2;

Qy         11 SISWAIFTGLAALCLFQGVPVRSGDATFP-KAMDNVTVRQGESATLRCTIDNRVTRVAWL 69
              |  |     |   ||     : :    ||  | |:: ||:|:::| ||| :::  :: |||
Db         11 SHQWLAAVLLGLCCLLPAGRLAAPGGDFPGAAADSLVVRKGDTAVLRCYLEDGASKGAWL 70

Qy         70 NRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRVH 129
              |||:|:::||:||| :|||| : :  : :||::||:||| |:|||||||| : |:| :||
Db         71 NRSSIIFAGSDKWSVDPRVSIATANRREYSLQIQDVDVTDDGPYTCSVQTQHTPRTMQVH 130

Qy        130 LIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEIQ 189
              | |||||||  ||||| :|||:|::| |:|||:|||:::|||||| |  | |  :||:|
Db        131 LTVQVSPKIFRISSDIVVNEGSNVTLVCLATGKPEPSISWRHISPSAKPFES-GQYLDIY 189

Qy        190 GITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVP 249
              ||||:|:|:||||| ||||: | |::|||||: | | | | :|| :|  | ::|| : ||
Db        190 GITRDQAGEYECSAENDVSVPDVKKVKVTVNFAPTIQELKSSGVMLGGNGLIRCEGAGVP 249

Qy        250 SAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIM 309
              :  |:||: :::|| |::|: ::|    | |   ||:|  :|||||||:|||| ||||:
Db        250 APVFEWYRGERKLISGQQGITIKNYSTRSLLTVTNVTEEHFGNYTCVAANKLGMTNASLP 309

Qy        310 LFGPGAVSEVSNGTSRRAGCVWLLPLLVLHL 340
              | |       | :      | | | :  |
Db        310 LNPPSTAQYGITGDAEVLFSCWYLVLTLSSL 340


RESULT 11
Q8NAQ3
ID   Q8NAQ3      PRELIMINARY;      PRT;  354 AA.
AC   Q8NAQ3;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein FLJ34988.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Nishi T., Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H.,
RA   Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
RA   Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA   Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,
RA   Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K.,
RA   Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,
RA   Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK092307; BAC03858.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00408; IGc2; 3.
DR   PROSITE; PS50835; IG_LIKE; 3.
KW   Hypothetical protein; Immunoglobulin domain.
SQ   SEQUENCE   354 AA;  38779 MW;  5DC938094E35964A CRC64;
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  Query Match           52.4%;  Score 946;  DB 7;  Length 334;
  Best Local Similarity  55.2%;  Pred. No. 6.7e-72;
  Matches  182;  Conservative   57;  Mismatches   85;  Indels    6;  Gaps    4;

Qy         14 WAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRST 73
              |  :  |       |||:|||| |  | :  ||:|||||::| ||| :::| ::|||||||
Db         10 WVL--GFFLFLFFQGLPVRSVD--FTRGTDNITVRQGDTAILRCFVEDRSSKVAWLNRSG 65

Qy         74 ILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQ 133
              |::|| ||| ||||| |  :  :||: || ||||||| ||||||| :|||||:|:|||||
Db         66 IIFAGEDKWSLDPRVELEKRSPLEYSLRIQKVDVYDEGSYTCSVQTQHHPKTSQVYLIVQ 125

Qy        134 VSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEIQGITR 193
              |.|||  |||||::|||:|::| |:| ||||| :||||::|    |  |:|||||| ||||
Db        126 VPPKISNISSDITVNEGSNVTLVCMANGRPEPVITWRHLTPTGKEFEGEEEYLEILGITR 185

Qy        194 EQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEF 253
              |||| ||| |:|:|||:  |::|:|||||||| |:|:|      |::  |:||||||: :|
Db        186 EQSGKYECKAANEVASADVKQVRVTVNYPPTITESKSNEAATGRQALLRCEASAVPTPDF 245

Qy        254 QWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIMLFGP 313
              :||:|| | |    |:::::    | |:  ||:|  |||||||:|||| |||| |: |
Db        246 EWYRDDTR-INSANGLEIKSTGSQSLLMVANVTEEHYGNYTCVAANKLGVTNASLYLYRP 304

Qy        314 GAVSEVSNGTSRRAGCVWLLPLLVLHLLLK 343
              |    | |||:   |  :|||   :| || |
Db        305 G-TGRVDNGSVSLAVPLWLLAASLLCLLSK 333


RESULT 7
Q8IV49
ID   Q8IV49      PRELIMINARY;      PRT;   338 AA.
AC   Q8IV49;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Similar to limbic system-associated membrane protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Colon;
RA   Strausberg R.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC033803; AAH33803.1; -.
SQ   SEQUENCE   338 AA;  37393 MW;  88CF00E07302817B CRC64;

  Query Match           51.6%;  Score 932.5;  DB 4;  Length 338;
  Best Local Similarity  55.4%;  Pred. No. 9.5e-71;
  Matches  180;  Conservative   60;  Mismatches   80;  Indels    5;  Gaps    4;

Qy         20 LAALCLF-QGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTILYAG 78
              |  |||   |:|||| |  | :  ||:|||||::| ||| :::: ::|||||| |::||
Db         17 LRLLCLLPTGLPVRSVD--FNRGTDNITVRQGDTAILRCVVEDKNSKVAWLNRSGIIFAG 74

Qy         79 NDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKI 138
              :||| ||||| |      :||: || ||||||| ||||||| : ||||:|:|||| |||
Db         75 HDKWSLDPRVELEKRHSLEYSLRIQKVDVYDEGSYTCSVQTQHEPKTSQVYLIVQVPPKI 134

Qy        139 VEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEIQGITREQSGD 198
              |||||::|||:|::| |:| ||||| :||||::|    |  |:|||| ||||||||
Db        135 SNISSDVTVNEGSNVTLVCMANGRPEPVITWRHLTPTGREFEGEEEYLEILGITREQSGK 194

Qy        199 YECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWYKD 258
              ||| |:|:|::  |::|||||||| |:|:|      |:: :|:|||||: :|:||:|
Db        195 YECKAANEVSSADVKQVKVTVNYPPTITESKSNEATTGRQASLKCEASAVPAPDFEWYRD 254

Qy        259 DKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIMLFGPGAVSE 318
              | | |    |:::::    | |   ||:|  ||||||||:|||| ||||::|| ||:|
Db        255 DTR-INSANGLEIKSTEGQSSLTVTNVTEEHYGNYTCVAANKLGVTNASLVLFRPGSVRG 313

Qy        319 VSNGTSRRAGCVWLLPLLVLHLLLK 343
              : ||:   |  :|||   :| || |
Db        314 I-NGSISLAVPLWLLAASLLCLLSK 337


RESULT 8
O02869
ID   O02869      PRELIMINARY;      PRT;   350 AA.
AC   O02869;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   ChLAMP, g11-isoform precursor.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=97358596; PubMed=9215692;
RA   Bruemmendorf T., Spaltmann F., Treubert U.;
RT   "Cloning and characterization of a neural cell recognition molecule on
RT   axons of the retinotectal system and spinal cord.";
RL   Eur. J. Neurosci. 9:1105-1116(1997).
DR   EMBL; Z94719; CAB08114.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2;
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00408; IGc2; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
KW   Brain; GPI-anchor; Immunoglobulin domain; Signal.
FT   SIGNAL        1     28       POTENTIAL.
FT   CHAIN        29    350       CHLAMP, G11-ISOFORM.
SQ   SEQUENCE   350 AA;  38656 MW;  0844A892878894D4 CRC64;

  Query Match           51.5%;  Score 930.5;  DB 7;  Length 350;
  Best Local Similarity  54.3%;  Pred. No. 1.5e-70;
  Matches  183;  Conservative   56;  Mismatches   81;  Indels   17;  Gaps    5;

Qy         20 LAALCLF-QGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTILYAG 78
              |  |||   |:|||| |  | :  ||:|||||::| ||| :::| ::|||||| |::||
Db         17 LRLLCLLPTGLPVRSVD--FTRGTDNITVRQGDTAILRCFVEDRSSKVAWLNRSGIIFAG 74

Qy         79 NDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKI 138
              ||| ||||| |  :  :||: || ||||||| ||||||| :|||||:|:||||| |||
Db         75 EDKWSLDPRVELEKRSPLEYSLRIQKVDVYDEGSYTCSVQTQHHPKTSQVYLIVQVPPKI 134

Qy        139 VEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEIQGITREQSGD 198
              |||||::|||:|::| |:| ||||| :||||::|    |  |:|||| ||||||||
Db        135 SNISSDITVNEGSNVTLVCMANGRPEPVITWRHLTPTGKEFEGEEEYLEILGITREQSGK 194

Qy        199 YECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWYKD 258
              ||| |:|:|::  |::|:|||||||| |:|:|      |::  |:||||||: :|:||:|
Db        195 YECKAANEVASADVKQVRVTVNYPPTITESKSNEAATGRQALLRCEASAVPTPDFEWYRD 254

Qy        259 DKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIMLF------- 311
              | | |    |:::::    | |:  ||:|  |||||||:|||| ||||: |:
Db        255 DTR-INSANGLEIKSTGSQSLLMVANVTEEHYGNYTCVAANKLGVTNASLYLYKRVLPTL 313

Qy        312 -----GPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLK 343
                  |||   | ||:   |  :|||   :| || |
Db        314 PNPFPGPG-TGRVDNGSVSLAVPLWLLAASLLCLLSK 349


RESULT 9
Q8BLK3
ID   Q8BLK3      PRELIMINARY;      PRT;   341 AA.
AC   Q8BLK3;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
```

```
DE   CEPU-Se alpha 1 isoform.
GN   CEPU-SE.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Lodge A.P., McNamee C.J., Howard M.R., Reed J.E., Moss D.J.;
RT   "Characterisation of CEPU-Se, a secreted isoform of the IgLON family
RT   protein CEPU-1.";
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF292936; AAG01879.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00408; IGc2; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
KW   Immunoglobulin domain.
SQ   SEQUENCE   315 AA;  34606 MW;  68C5D27F0DDC6FB2 CRC64;

  Query Match           75.2%;  Score 1357.5;  DB 13;  Length 315;
  Best Local Similarity  83.0%;  Pred. No. 8.5e-107;
  Matches  253;  Conservative   26;  Mismatches   23;  Indels    3;  Gaps    1;

Qy       11 SISWAIFTGLAALCLF---QGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVA 67
           :: |    |    ||    ||||||||||||||||||||||||||||||::|||||||
Db        8 ALPWRCLVVLCLRLLFLVPAGVPVRSGDATFPKAMDNVTVRQGESATLRCSVDNRVTRVA 67

Qy       68 WLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSR 127
           |||||:|||||||||||||||||:||:|||||:| :|||||||||||||||||||||||
Db       68 WLNRSSILYAGNDKWCLDPRVVLLANTKTQYSIQIHDVDVYDEGPYTCSVQTDNHPKTSR 127

Qy      128 VHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLE 187
           |||||||||| |||||||||| |:||||||||||:||:|||||||||||:|||||||
Db      128 VHLIVQVSPKITEISSDISINEGGNVSLTCIATGRPDPTITWRHISPKAVGFISEDEYLE 187

Qy      188 IQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASA 247
           | ||||||||:|||||||||||||||:|||||||||||||:|| |||||||| | |||||
Db      188 ITGITREQSGEYECSASNDVAAPVVQRVKVTVNYPPYISDAKSTGVPVGQKGILMCEASA 247

Qy      248 VPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNAS 307
           ||||:|||||||||| ||:||:||||: | |:| |||||| |||||||||||:||:||||
Db      248 VPSADFQWYKDDKRLAEGQKGLKVENKAFFSRLTFFNVSEQDYGNYTCVASNQLGNTNAS 307

Qy      308 IMLFG 312
           ::|:|
Db      308 MILYG 312


RESULT 5
Q9DF61
ID   Q9DF61      PRELIMINARY;      PRT;   344 AA.
AC   Q9DF61;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   OBCAM alpha 1 isoform.
GN   OBCAM.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=20499204; PubMed=11042360;
RA   Lodge A.P., Howard M.R., McNamee C.J., Moss D.J.;
RT   "Co-localisation, heterophilic interactions and regulated expression
RT   of IgLON family proteins in the chick nervous system.";
RL   Brain Res. Mol. Brain Res. 82:84-94(2000).
DR   EMBL; AF292934; AAG01877.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00408; IGc2; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
KW   Immunoglobulin domain.
SQ   SEQUENCE   344 AA;  37531 MW;  37FE6051CBF0E7B4 CRC64;

  Query Match           70.6%;  Score 1275.5;  DB 13;  Length 344;
  Best Local Similarity  72.8%;  Pred. No. 8.5e-100;
  Matches  246;  Conservative   32;  Mismatches   53;  Indels    7;  Gaps    3;

Qy       12 ISWAIFTGLAALCLF---QGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAW 68
           : |    |    ||    |||||||||||||||||||||||||||||:|:|| ||||
Db        9 LPWRCLVVLCLRLLFLVPAGVPVRSGDATFPKAMDNVTVRQGESATLRCTVDDRVRRVAW 68

Qy       69 LNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRV 128
           |||||||||||||| :| |||:||||:|||||:| |||||||||||||||||||||||||
Db       69 LNRSTILYAGNDKWSIDNRVVILSNTKTQYSIKIHNVDVYDEGPYTCSVQTDNHPKTSRV 128

Qy      129 HLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEI 188
           |||||| |:|| |||||::|||::::| |:| ||||||||||:| |  ||||||||||
Db      129 HLIVQVPPQIVNISSDITVNEGSSVTLMCLAFGRPEPTVTWRHLSGKGQGFVSEDEYLEI 188

Qy      189 QGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAV 248
           |||||||:||||| |||| | ||:||||||||||||| || ||  ||||| ||||||||
Db      189 TGITREQSGEYECSAVNDVAVPDVRKVKVTVNYPPYISNAKNTGASVGQKGILQCEASAV 248

Qy      249 PSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASI 308
           | |||||:|:| ||  | :||::|::  || | |||||| |||||||||:||||:|||||
Db      249 PVAEFQWFKEDTRLANGLEGVRIESKGRLSTLTFFNVSEKDYGNYTCVATNKLGNTNASI 308

Qy      309 MLFGPGAVSEVSNGTSRRAG--CVWLLPLLVLHLLLKF 344
           :|:||||| :  |  || |   |:|.   |:  ||| |
Db      309 ILYGPGAVHDSGNAASRAAAGLCLW--ATLLARLLLDF 344


RESULT 6
O02870
ID   O02870      PRELIMINARY;      PRT;   334 AA.
AC   O02870;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   ChLAMP, g9-isoform precursor.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=97358596; PubMed=9215692;
RA   Bruemmendorf T., Spaltmann F., Treubert U.;
RT   "Cloning and characterization of a neural cell recognition molecule on
RT   axons of the retinotectal system and spinal cord.";
RL   Eur. J. Neurosci. 9:1105-1116(1997).
DR   EMBL; Z94718; CAB08113.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00408; IGc2; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
KW   Brain; GPI-anchor; Immunoglobulin domain; Signal.
FT   SIGNAL       1     24       POTENTIAL.
FT   CHAIN       25    334       CHLAMP, G9-ISOFORM.
SQ   SEQUENCE   334 AA;  37288 MW;  0B40A768D9609E77 CRC64;
```

```
Db        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180

Qy        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240
              ||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||
Db        181 SEDEYLEIQGITREQSGEYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240

Qy        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300
              |||||||||||||||:||||||:||||||||||||||||| ||||||||||||||||||||
Db        241 LQCEASAVPSAEFQWFKDDKRLVEGKKGVKVENRPFLSKLTFFNVSEHDYGNYTCVASNK 300

Qy        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
              ||||||||||||||||||:|||||||||:|||||||||||||||
Db        301 LGHTNASIMLFGPGAVSEVNNGTSRRAGCIWLLPLLVLHLLLKF 344


RESULT 2
O57596
ID   O57596      PRELIMINARY;      PRT;   313 AA.
AC   O57596;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Neural secreted glycoprotein (CEPU-SE alpha 2 isoform).
GN   CEPU OR CEPU-SE.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kim D., Moss D.J.;
RL   Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Lodge A.P., McNamee C.J., Howard M.R., Reed J.E., Moss D.J.;
RT   "Characterisation of CEPU-Se, a secreted isoform of the IgLON family
RT   protein CEPU-1.";
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ225897; CAA12649.1; -.
DR   EMBL; AF292935; AAG01878.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00408; IGc2; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
KW   Immunoglobulin domain.
SQ   SEQUENCE   313 AA;  34482 MW;  99AD825CAE4A5347 CRC64;

  Query Match          79.1%;  Score 1428;  DB 13;  Length 313;
  Best Local Similarity   85.4%;  Pred. No. 9e-113;
  Matches  263;  Conservative   27;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          5 QPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVT 64
              | || : :|| || |:||| |||||||||||||||||||||||||||||||::||||||
Db          3 QAKMQHPVSWVIFAGMAALLLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCSVDNRVT 62

Qy         65 RVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPK 124
              ||||||||:|||||||||||||||||:||:||||||:| :|||||||||||||||||||
Db         63 RVAWLNRSSILYAGNDKWCLDPRVVLLANTKTQYSIQIHDVDVYDEGPYTCSVQTDNHPK 122

Qy        125 TSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDE 184
              |||||||||||||| |||||||||||:|||||||||:||:||||||||||||||||||||
Db        123 TSRVHLIVQVSPKITEISSDISINEGGNVSLTCIATGRPDPTITWRHISPKAVGFISEDE 182

Qy        185 YLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCE 244
              |||| |||||||||:|||||||||||||||:|||||||||||||:|| ||||||||| | ||
Db        183 YLEITGITREQSGEYECSASNDVAAPVVQRVKVTVNYPPYISDAKSTGVPVGQKGILMCE 242

Qy        245 ASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHT 304
              |||||||:|||||||||| ||:||:||||: | |:| ||||||.||||||||||:|:||:|

Db        243 ASAVPSADFQWYKDDKRLAEGQKGLKVENKAFFSRLTFFNVSEQDYGNYTCVAS
Qy        305 NASIMLFG 312
              |||::|:|
Db        303 NASMILYG 310


RESULT 3
O93242
ID   O93242      PRELIMINARY;      PRT;   344 AA.
AC   O93242;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   CEPU-1.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kimura Y., Shirabe K., Fukushima M., Takeshita M., Tanaka H.;
RT   "CEPU-1: an Immunoglobulin Superfamily Molecule, Has Cell Adhesion
RT   Activity and Shows Dynamic Expression Patterns in Chick Embryonic
RT   Spinal Cord.";
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB011810; BAA31514.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00408; IGc2; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
KW   Immunoglobulin domain.
SQ   SEQUENCE   344 AA;  37613 MW;  22CAA8F526A6B57E CRC64;

  Query Match          79.0%;  Score 1427.5;  DB 13;  Length 344;
  Best Local Similarity   79.2%;  Pred. No. 1.1e-112;
  Matches  267;  Conservative   31;  Mismatches   36;  Indels    3;  Gaps    1;

Qy         11 SISWAIFTGLAALCLF---QGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVA 67
              :: |    |    ||    |||||||||||||||||||||||||||::||||||||
Db          8 ALPWRCLVVLCLRLLFLVPAGVPVRSGDATFPKAMDNVTVRQGESATLRCSVDNRVTRVA 67

Qy         68 WLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSR 127
              |||||:||||||||||||||||:||:||||||:| :|||||||||||||||||||||||
Db         68 WLNRSSILYAGNDKWCLDPRVVLLANTKTQYSIQIHDVDVYDEGPYTCSVQTDNHPKTSR 127

Qy        128 VHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLE 187
              |||||||||| |||||||||| |:||||||||||:||:||||||||||||||||||||||
Db        128 VHLIVQVSPKITEISSDISINEGGNVSLTCIATGRPDPTITWRHISPKAVGFISEDEYLE 187

Qy        188 IQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASA 247
              | ||||||:||||||||||||:||||||||||||:|| |||||||| | |||||
Db        188 ITGITREQSGEYECSASNDVAAPVVQRVKVTVNYPPYISDAKSTGVPVGQKGILMCEASA 247

Qy        248 VPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNAS 307
              ||||:|||||||||| ||:||:||||: | |:| |||||| ||||||||||:||:|||||
Db        248 VPSADFQWYKDDKRLAEGQKGLKVENKAFFSRLTFFNVSEQDYGNYTCVASNQLGNTNAS 307

Qy        308 IMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
              ::|:|||||| : ::|  ||  | ||| | :  |  :|
Db        308 MILYGPGAVHDGNSGAWRRGSCAWLLALPLAQLARQF 344


RESULT 4
Q9DGI5
ID   Q9DGI5      PRELIMINARY;      PRT;   315 AA.
AC   Q9DGI5;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 11, 2003, 03:01:28 ; Search time 78 Seconds
(without alignments)
1138.078 Million cell updates/sec

Title: US-10-017-084A-523
Perfect score: 1806
Sequence: 1 MKTIQPKMHNSISWAIFTGL.....RRAGCVWLLPLLVLHLLLKF 344

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1780	98.6	344	11	Q8BG33	Q8bg33 mus musculu
2	1428	79.1	313	13	O57596	O57596 gallus gall
3	1427.5	79.0	344	13	O93242	O93242 gallus gall
4	1357.5	75.2	315	13	Q9DGI5	Q9dgi5 gallus gall
5	1275.5	70.6	344	13	Q9DF61	Q9df61 gallus gall
6	945	52.4	334	7	O02870	O02870 gallus gall
7	932.5	51.6	338	4	Q8IV49	Q8iv49 homo sapien
8	930.5	51.5	350	7	O02869	O02869 gallus gall
9	894	49.5	341	11	Q8BLK3	Q8blk3 mus musculu
10	842	46.6	352	13	Q9W6V2	Q9w6v2 gallus gall
11	820	45.4	354	4	Q8NAQ3	Q8naq3 homo sapien
12	759	42.0	325	7	Q8HW98	Q8hw98 mus musculu
13	686.5	38.0	188	11	Q8BMT5	Q8bmt5 mus musculu
14	599	33.2	261	13	Q9W6V1	Q9w6v1 gallus gall
15	545.5	30.2	226	4	Q8N440	Q8n440 homo sapien
16	380.5	21.1	606	5	Q9VMN6	Q9vmn6 drosophila
17	350.5	19.4	672	5	Q8IP70	Q8ip70 drosophila
18	348	19.3	554	5	Q9W4R3	Q9w4r3 drosophila
19	338.5	18.7	413	5	Q9VAR6	Q9var6 drosophila
20	333	18.4	315	5	Q9VMB2	Q9vmb2 drosophila
21	308.5	17.1	528	5	P91670	P91670 drosophila
22	306	16.9	545	5	Q9VCT4	Q9vct4 drosophila
23	303.5	16.8	316	5	Q8WPB3	Q8wpb3 drosophila
24	301	16.7	526	5	Q9VMN9	Q9vmn9 drosophila
25	300.5	16.6	316	5	Q8WP94	Q8wp94 drosophila
26	297.5	16.5	316	5	Q8WP58	Q8wp58 drosophila
27	290.5	16.1	2673	4	Q96SC3	Q96sc3 homo sapien
28	290.5	16.1	5636	4	Q96RW7	Q96rw7 homo sapien
29	287	15.9	846	13	O57577	O57577 cynops pyrr
30	287	15.9	1100	13	O57576	O57576 cynops pyrr
31	285.5	15.8	373	5	Q9VLF0	Q9vlf0 drosophila
32	285.5	15.8	603	5	Q9NKF5	Q9nkf5 drosophila
33	284	15.7	403	5	Q9VP08	Q9vp08 drosophila
34	282.5	15.6	605	11	Q921P2	Q921p2 mus musculu
35	282.5	15.6	838	11	Q8C4B2	Q8c4b2 mus musculu
36	282.5	15.6	838	11	Q8BQ96	Q8bq96 mus musculu
37	279.5	15.5	725	13	O73633	O73633 xenopus lae
38	278.5	15.4	4162	13	Q98918	Q98918 gallus gall
39	273.5	15.1	725	13	O73634	O73634 xenopus lae
40	272.5	15.1	1323	13	Q08476	Q08476 gallus gall
41	269.5	14.9	484	5	Q26475	Q26475 schistocerc
42	268.5	14.9	1496	4	Q92626	Q92626 homo sapien
43	265	14.7	1482	5	Q9V4Y0	Q9v4y0 drosophila
44	261.5	14.5	437	4	Q8IZP8	Q8izp8 homo sapien
45	261	14.5	1031	13	Q90YM2	Q90ym2 brachydanio

ALIGNMENTS

RESULT 1
Q8BG33
ID Q8BG33 PRELIMINARY; PRT; 344 AA.
AC Q8BG33;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Neurotrimin precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK045973; BAC32555.1; -.
DR EMBL; AK046377; BAC32695.1; -.
SQ SEQUENCE 344 AA; 37941 MW; CDA5299D4CD86065 CRC64

Query Match 98.6%; Score 1780; DB 11; Le
Best Local Similarity 98.0%; Pred. No. 1.6e-142;
Matches 337; Conservative 5; Mismatches 2;

Qy 1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPK
||||| |||||||||||||||||||||||||||||||||
Db 1 MKTIQAKMHNSISWAIFTGLAALCLFQGVPVRSGDATFI

Qy 61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQ
||||||||||||||||||||||||||||||||||||
Db 61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQT

Qy 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNIS
|||||||||||||||||||||||||||||||||||

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FT   DISULFID     139    189       PROBABLE.
FT   DISULFID     235    288       PROBABLE.
FT   DISULFID     330    386       PROBABLE.
FT   DISULFID     427    480       PROBABLE.
FT   CARBOHYD     222    222       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     316    316       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     348    348       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     424    424       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     450    450       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     479    479       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC     810   1076       Missing (in isoform N-CAM 140).
FT                                 /FTId=VSP_002588.
SQ   SEQUENCE   1115 AA;  119351 MW;  2C93DCD474CFBCAF CRC64;

  Query Match             15.7%;  Score 283.5;  DB 1;  Length 1115;
  Best Local Similarity   25.8%;  Pred. No. 1.6e-14;
  Matches   75;  Conservative   45;  Mismatches  130;  Indels   41;  Gaps    7;

Qy         44 NVTVRQGESATLRCTIDNRVTRVAWLNRSTILYAGNDKWCLDPRVV--------LLSNTQ 95
              | |    |:| || |  |                 |:       | |    :        |:
Db        222 NATANLGQSVTLVCDADG-------FPEPTM------SWTKDGEPIENEEEDERSRSSVS 268

Qy         96 TQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNNISL 155
                    : |:|||  ||  | |   :      : : :|| |   |||  : :  ::      ::|
Db        269 DSSEVTIRNVDKNDEAEYVCIAENKAGEQDASIHLKVFAKPKITYVENQTAMELEEQVTL 328

Qy        156 TCIATGRPEPTVTWR---------------HISPKAVGFVSEDEYLEIQGITREQSGDYE 200
              || |:| | |::|||               |:  ::    ||     | :: |      :|:|
Db        329 TCEASGDPIPSITWRTSTRNISSEEQDLDGHMVVRSHARVSS---LTLKSIQYRDAGEYM 385

Qy        201 CSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWYKDDK 260
              |:||| :      : : :   | | :           | :   : ||  | |||   |::|: :
Db        386 CTASNTIGQD-SQSIDLEFQYAPKLQGPVAVYTWEGNQVNITCEVFAYPSATISWFRDGQ 444

Qy        261 RLIEGK-KGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIML 310
               |         :|: | |  | |        ||:|:||| | | |::|  :   :|
Db        445 LLPSSNYSNIKIYNTPSASYLEVTPDSENDFGNYNCTAVNRIGQESLEFIL 495

Search completed: September 11, 2003, 03:03:27
Job time : 36 secs
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  Matches   75;  Conservative   45;  Mismatches  130;  Indels   41;  Gaps    7;

Qy         44 NVTVRQGESATLRCTIDNRVTRVAWLNRSTILYAGNDKWCLDPRVV--------LLSNTQ 95
              | |   |:| || |  |            |:       |  |   :          |:
Db        222 NATANLGQSVTLVCDADG-------FPEPTM------SWTKDGEPIENEEEDERSRSSVS 268

Qy         96 TQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNNISL 155
                  : |:|||  ||  | |  :     : : :|| |   |||  : :  ::     ::|
Db        269 DSSEVTIRNVDKNDEAEYVCIAENKAGEQDASIHLKVFAKPKITYVENQTAMELEEQVTL 328

Qy        156 TCIATGRPEPTVTWR---------------HISPKAVGFVSEDEYLEIQGITREQSGDYE 200
              || |:| | |::|||               |:  ::  ||     | :: |    :|:|
Db        329 TCEASGDPIPSITWRTSTRNISSEEQDLDGHMVVRSHARVSS---LTLKSIQYRDAGEYM 385

Qy        201 CSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWYKDDK 260
              |:||| :     : : :   | | :          | :  : ||  | |||   |::| :
Db        386 CTASNTIGQD-SQSIDLEFQYAPKLQGPVAVYTWEGNQVNITCEVFAYPSATISWFRDGQ 444

Qy        261 RLIEGK-KGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIML 310
               |       :|: | | | |      ||:|:||| | | |::|  :   :|
Db        445 LLPSSNYSNIKIYNTPSASYLEVTPDSENDFGNYNCTAVNRIGQESLEFIL 495
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RESULT 15
NCA1_MOUSE
ID   NCA1_MOUSE     STANDARD;      PRT;  1115 AA.
AC   P13595; Q61949;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Neural cell adhesion molecule 1, 180 kDa isoform precursor (N-CAM 180)
DE   (NCAM-180).
GN   NCAM1 OR NCAM.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM N-CAM 180).
RC   STRAIN=C57BL/6;
RX   MEDLINE=87246524; PubMed=3595563;
RA   Barthels D., Santoni M.J., Wille W., Ruppert C., Chaix J.C.,
RA   Hirsch M.R., Fontecilla-Camps J.C., Goridis C.;
RT   "Isolation and nucleotide sequence of mouse NCAM cDNA that codes for
RT   a Mr 79,000 polypeptide without a membrane-spanning region.";
RL   EMBO J. 6:907-914(1987).
RN   [2]
RP   SEQUENCE OF 529-1115 FROM N.A. (ISOFORM N-CAM 140).
RC   STRAIN=C57BL/6;
RX   MEDLINE=88067687; PubMed=3684567;
RA   Santoni M.-J., Barthels D., Barbas J.A., Hirsch M.-R., Steinmetz M.,
RA   Goridis C., Wille W.;
RT   "Analysis of cDNA clones that code for the transmembrane forms of the
RT   mouse neural cell adhesion molecule (NCAM) and are generated by
RT   alternative RNA splicing.";
RL   Nucleic Acids Res. 15:8621-8641(1987).
RN   [3]
RP   SEQUENCE OF 642-1115 FROM N.A. (ISOFORM N-CAM 180).
RX   MEDLINE=88283628; PubMed=3396534;
RA   Barbas J.A., Chaix J.C., Steinmetz M., Goridis C.;
RT   "Differential splicing and alternative polyadenylation generates
RT   distinct NCAM transcripts and proteins in the mouse.";
RL   EMBO J. 7:625-632(1988).
RN   [4]
RP   SEQUENCE OF 804-1081 FROM N.A. (ISOFORM N-CAM 180).
RC   STRAIN=C57BL/6J; TISSUE=Brain;
RX   MEDLINE=88247737; PubMed=2454455;
RA   Barthels D., Vopper G., Wille W.;
RT   "NCAM-180, the large isoform of the neural cell adhesion molecule of
RT   the mouse, is encoded by an alternatively spliced transcript.";
RL   Nucleic Acids Res. 16:4217-4225(1988).
RN   [5]
RP   SEQUENCE OF 702-1115 FROM N.A. (ISOFORM N-CAM 140).
RC   STRAIN=C57BL/6; TISSUE=Brain;
RX   MEDLINE=89251563; PubMed=2721486;
RA   Santoni M.J., Barthels D., Vopper G., Boned A., Goridis C., Wille M.;
RT   "Differential exon usage involving an unusual splicing mechanism
RT   generates at least eight types of NCAM cDNA in mouse brain.";
RL   EMBO J. 8:385-392(1989).
RN   [6]
RP   SEQUENCE OF 20-36.
RX   MEDLINE=86140120; PubMed=3512556;
RA   Rougon G., Marshak D.R.;
RT   "Structural and immunological characterization of the amino-terminal
RT   domain of mammalian neural cell adhesion molecules.";
RL   J. Biol. Chem. 261:3396-3401(1986).
CC   -!- FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE INVOLVED IN
CC       NEURON-NEURON ADHESION, NEURITE FASCICULATION, OUTGROWTH OF
CC       NEURITES, ETC.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC       Name=N-CAM 180;
CC         IsoId=P13595-1; Sequence=Displayed;
CC       Name=N-CAM 140;
CC         IsoId=P13595-2; Sequence=VSP_002588;
CC       Name=N-CAM 120;
CC         IsoId=P13594-1; Sequence=External;
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC   -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
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CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; X07200; CAA30177.1; -.
DR   EMBL; Y00051; -; NOT_ANNOTATED_CDS.
DR   EMBL; X06328; CAA29641.1; -.
DR   EMBL; X07195; CAA30173.1; -.
DR   EMBL; X07244; CAA30230.1; -.
DR   EMBL; X15051; CAA33150.1; -.
DR   EMBL; X15052; CAA33151.1; -.
DR   PIR; A29673; IJMSNL.
DR   MGD; MGI:97281; Ncam1.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00041; fn3; 2.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00060; FN3; 2.
DR   SMART; SM00408; IGc2; 5.
DR   PROSITE; PS50835; IG_LIKE; 5.
KW   Cell adhesion; Glycoprotein; Transmembrane; Repeat;
KW   Immunoglobulin domain; Alternative splicing; Signal; Heparin-binding.
FT   SIGNAL        1     19
FT   CHAIN        20   1115       NEURAL CELL ADHESION MOLECULE 1, 180 kDa
FT                                ISOFORM.
FT   DOMAIN       20    711       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    712    729       POTENTIAL.
FT   DOMAIN      730   1115       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       20    111       IG-LIKE C2-TYPE 1.
FT   DOMAIN      116    205       IG-LIKE C2-TYPE 2.
FT   DOMAIN      212    302       IG-LIKE C2-TYPE 3.
FT   DOMAIN      309    402       IG-LIKE C2-TYPE 4.
FT   DOMAIN      407    492       IG-LIKE C2-TYPE 5.
FT   DOMAIN      519    596       FIBRONECTIN TYPE-III 1.
FT   DOMAIN      625    692       FIBRONECTIN TYPE-III 2.
FT   DOMAIN      152    156       HEPARIN-BINDING (POTENTIAL).
FT   DOMAIN      161    165       HEPARIN-BINDING (POTENTIAL).
FT   DISULFID     41     96       PROBABLE.
```

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Qy          44 NVTVRQGESATLRCTIDN-RVTRVAWLNR-------STILYAGNDKWCLDPR--VVLLSN 93
               :|    |:|    ||::     |:|  |       | :|   |    | |  | :
Db          33 DVVASVGDSVEFNCTVEEVGQLSVSWAKRPSESDTNSVVLSMRNILSLPDQRYNVTVTEG 92

Qy          94 TQTQ---YSIEIQNVDVYDEGPYTCSVQTDNHPK-TSRVHLIVQVSPKIVE-ISSDISIN 148
                :|    |:  ||||::| | ||| | |      | | :: | ::  | | |       :
Db          93 PKTGSAIYTFRIQNIEVSDMGPYECQVLVSATEKVTKKLSLQIKTPPVIAENTPKSTLVT 152

Qy         149 EGNNISLTCIATGRPEPTVTWRH----ISPKAVGFVSEDEYLEIQGITREQSGDYECSAS 204
               || |: ||| | | |:||::|     : | | | :  :  | |: : |  | | | |
Db         153 EGQNLELTCHANGFPKPTISWAREHNAVMP-AGGHLLAEPTLRIRSVHRMDRGGYYCIAQ 211

Qy         205 NDVAAPVVRRVKVTVNYPPYIS-EAKGTGVPVGQKGTLQCEASAVPSAEFQWYKDDKRLI 263
               |    |  | ::| | : | |: :       |     |:|     |:    |:|:   |
Db         212 NGEGQPDKRLIRVEVEFRPQIAVQRPKIAQMVSHSAELECSVQGYPAPTVVWHKNGVPL- 270

Qy         264 EGKKGVKVENR-----PFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIMLF 311
               :  :  :| |         | |   :| | |:|:| | |:||||| :| : ||
Db         271 QSSRHHEVANTASSSGTTTSVLRIDSVGEEDFGDYYCNATNKLGHADARLHLF 323


RESULT 14
NCA2_MOUSE
ID   NCA2_MOUSE     STANDARD;      PRT;   725 AA.
AC   P13594; Q61950;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Neural cell adhesion molecule 1, 120 kDa isoform precursor (N-CAM 120)
DE   (NCAM-120).
GN   NCAM1 OR NCAM.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=87246524; PubMed=3595563;
RA   Barthels D., Santoni M.-J., Wille W., Ruppert C., Caix J.-C.,
RA   Hirsch M.-R., Fontecilla-Camps J.-C., Goridis C.;
RT   "Isolation and nucleotide sequence of mouse NCAM cDNA that codes for
RT   a Mr 79,000 polypeptide without a membrane-spanning region.";
RL   EMBO J. 6:907-914(1987).
RN   [2]
RP   SEQUENCE OF 20-700 FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RX   MEDLINE=89251563; PubMed=2721486;
RA   Santoni M.J., Barthels D., Vopper G., Boned A., Goridis C., Wille M.;
RT   "Differential exon usage involving an unusual splicing mechanism
RT   generates at least eight types of NCAM cDNA in mouse brain.";
RL   EMBO J. 8:385-392(1989).
RN   [3]
RP   SEQUENCE OF 642-725 FROM N.A.
RX   MEDLINE=88283628; PubMed=3396534;
RA   Barbas J.A., Chaix J.C., Steinmetz M., Goridis C.;
RT   "Differential splicing and alternative polyadenylation generates
RT   distinct NCAM transcripts and proteins in the mouse.";
RL   EMBO J. 7:625-632(1988).
RN   [4]
RP   SEQUENCE OF 20-36.
RX   MEDLINE=86140120; PubMed=3512556;
RA   Rougon G., Marshak D.R.;
RT   "Structural and immunological characterization of the amino-terminal
RT   domain of mammalian neural cell adhesion molecules.";
RL   J. Biol. Chem. 261:3396-3401(1986).
CC   -!- FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE INVOLVED IN
CC       NEURON-NEURON ADHESION, NEURITE FASCICULATION, OUTGROWTH OF
CC       NEURITES, ETC.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC       Name=N-CAM 120;
CC         IsoId=P13594-1; Sequence=Displayed;
CC       Name=N-CAM 180;
CC         IsoId=P13595-1; Sequence=External;
CC       Name=N-CAM 140;
CC         IsoId=P13595-2; Sequence=External;
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC   -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y00051; CAA68263.1; -.
DR   EMBL; X15049; CAA33148.1; ALT_SEQ.
DR   EMBL; X07195; CAA30173.1; -.
DR   PIR; A29673; IJMSNG.
DR   PDB; 2NCM; 12-MAR-97.
DR   PDB; 3NCM; 23-JUL-99.
DR   MGD; MGI:97281; Ncam1.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00041; fn3; 2.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00060; FN3; 2.
DR   SMART; SM00408; IGc2; 5.
DR   PROSITE; PS50835; IG_LIKE; 5.
KW   Cell adhesion; Glycoprotein; Repeat; Alternative splicing;
KW   Immunoglobulin domain; Signal; Heparin-binding; GPI-anchor;
KW   3D-structure.
FT   SIGNAL        1     19
FT   CHAIN        20    725       NEURAL CELL ADHESION MOLECULE 1, 120 kDa
FT                                 ISOFORM.
FT   DOMAIN       20    111       IG-LIKE C2-TYPE 1.
FT   DOMAIN      116    205       IG-LIKE C2-TYPE 2.
FT   DOMAIN      212    302       IG-LIKE C2-TYPE 3.
FT   DOMAIN      309    402       IG-LIKE C2-TYPE 4.
FT   DOMAIN      407    492       IG-LIKE C2-TYPE 5.
FT   DOMAIN      519    596       FIBRONECTIN TYPE-III 1.
FT   DOMAIN      625    692       FIBRONECTIN TYPE-III 2.
FT   DOMAIN      152    156       HEPARIN-BINDING (POTENTIAL).
FT   DOMAIN      161    165       HEPARIN-BINDING (POTENTIAL).
FT   DISULFID     41     96       PROBABLE.
FT   DISULFID    139    189       PROBABLE.
FT   DISULFID    235    288       PROBABLE.
FT   DISULFID    330    386       PROBABLE.
FT   DISULFID    427    480       PROBABLE.
FT   CARBOHYD    222    222       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    316    316       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    348    348       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    424    424       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    450    450       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    479    479       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    261    268       ERSRSSVS -> DEKHIFSD (IN REF. 2).
FT   CONFLICT    273    273       V -> L (IN REF. 2).
FT   CONFLICT    354    355       QD -> KT (IN REF. 2).
FT   CONFLICT    549    549       T -> K (IN REF. 2).
FT   CONFLICT    572    572       T -> R (IN REF. 2).
FT   CONFLICT    575    575       D -> V (IN REF. 2).
FT   CONFLICT    589    594       MQPSES -> SAATEF (IN REF. 2).
FT   CONFLICT    600    602       PEL -> REP (IN REF. 2).
FT   CONFLICT    657    657       H -> D (IN REF. 2 AND 3).
SQ   SEQUENCE   725 AA;  80296 MW;  C2AEB8B4461C6B2F CRC64;

  Query Match           15.7%;  Score 283.5;  DB 1;  Length 725;
  Best Local Similarity 25.8%;  Pred. No. 8.7e-15;
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Qy         68 WLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSR 127
              |||||:|::|| ||| :|||| : :  :  ||::|||||| |:|||||||| : |:| :
Db         65 WLNRSSIIFAGGDKWSVDPRVSISTLNKRDYSLQIQNVDVTDDGPYTCSVQTQHTPRTMQ 124

Qy        128 VHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLE 187
              ||| ||| ||| :||:|::|||| |::|||:|||:||| ::|||||| |  |    :||:
Db        125 VHLTVQVPPKIYDISNDMTINEGTNVTLTCLATGKPEPAISWRHISPSAKPF-ENGQYLD 183

Qy        188 IQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASA 247
              | ||||:|:|:||||| ||||: | |::|:| ||: | | | |  |  |: | ::|| :
Db        184 IYGITRDQAGEYECSAENDVSFPDVKKVRVVVNFAPTIQEIKSGTVTPGRSGLIRCEGAG 243

Qy        248 VPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNAS 307
              ||   |:||| :|||  |::|: ::|    | |   ||::  :||||||:|||| ||||
Db        244 VPPPAFEWYKGEKRLFNGQQGIIIQNFSTRSILTVTNVTQEHFGNYTCVAANKLGTTNAS 303

Qy        308 IMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
              : |  |       |::      | | | :  :: |
Db        304 LPLNPPSTAQYGITGSACDLFSCWSLALTLSSVISIF 340
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RESULT 13
AMAL_DROME
ID AMAL_DROME STANDARD; PRT; 333 AA.
AC P15364; Q9V3A5;
DT 01-APR-1990 (Rel. 14, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Amalgam protein precursor.
GN AMA OR BG:DS00276.6 OR CG2198.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Oregon-R;
RX MEDLINE=89028670; PubMed=3141062;
RA Seeger M.A., Haffley L., Kaufman T.C.;
RT "Characterization of amalgam: a member of the immunoglobulin
RT superfamily from Drosophila.";
RL Cell 55:589-600(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Celniker S.E., Pfeiffer B.D., Knafels J., Martin C.H., Mayeda C.A.,
RA Palazzolo M.J.;
RT "Complete sequence of the Antennapedia complex of Drosophila.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley; TISSUE=Embryo;
RX MEDLINE=22426066; PubMed=12537569;
RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
RA George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
RA Rubin G.M., Celniker S.E.;
RT "A Drosophila full-length cDNA resource.";
RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
CC (POSSIBLE).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC --
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CC --
DR EMBL; M23561; AAA28367.1; -.
DR EMBL; AE001572; AAD19797.1; -.
DR EMBL; AE003674; AAF54084.1; -.
DR EMBL; AY051911; AAK93335.1; -.
DR PIR; A31923; A31923.
DR FlyBase; FBgn0000071; Ama.
DR GO; GO:0005886; C:plasma membrane; IDA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00408; IGc2; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Immunoglobulin domain; Glycoprotein; GPI-anchor; Signal; Repeat.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 ? AMALGAM PROTEIN.
FT PROPEP ? 333 REMOVED IN MATURE FORM (POTENTIAL).
FT DOMAIN 25 128 IG-LIKE V-TYPE.
FT DOMAIN 139 223 IG-LIKE C2-TYPE 1.
FT DOMAIN 230 323 IG-LIKE C2-TYPE 2.
FT DISULFID 46 117 PROBABLE.
FT DISULFID 161 208 PROBABLE.
FT DISULFID 251 307 PROBABLE.
FT CARBOHYD 45 45 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 308 308 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 83 83 Q -> K (IN REF. 1).
SQ SEQUENCE 333 AA; 36387 MW; F644753DE3DB25F1 CRC64;

Query Match 16.5%; Score 297.5; DB 1; Length 333;
Best Local Similarity 29.7%; Pred. No. 2.4e-16;
Matches 87; Conservative 43; Mismatches 136; Indels 27; Gaps 11;

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CC       DETECTED IN PRESUMPTIVE CORTEX, MEDIAL LIMBIC AREAS OF THE
CC       THALAMUS AND HYPOTHALAMUS. IN THE ADULT, IT IS FOUND IN
CC       HYPOTHALAMUS, PERIRHINAL CORTEX, AMYGDALA AND MEDIAL THALAMIC
CC       REGION.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
CC       SUBFAMILY.
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U31554; AAA86120.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00408; IGc2; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
KW   Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
KW   Repeat; Signal.
FT   SIGNAL        1     28
FT   CHAIN        29    315       LIMBIC SYSTEM-ASSOCIATED MEMBRANE
FT                                 PROTEIN.
FT   PROPEP      316    338       REMOVED IN MATURE FORM (POTENTIAL).
FT   DOMAIN       29    122       IG-LIKE C2-TYPE 1.
FT   DOMAIN      132    214       IG-LIKE C2-TYPE 2.
FT   DOMAIN      219    304       IG-LIKE C2-TYPE 3.
FT   DISULFID     53    111       POTENTIAL.
FT   DISULFID    153    197       POTENTIAL.
FT   DISULFID    239    290       POTENTIAL.
FT   CARBOHYD     40     40       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     66     66       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    136    136       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    148    148       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    279    279       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    287    287       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    300    300       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    315    315       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   LIPID       315    315       GPI-ANCHOR (POTENTIAL).
SQ   SEQUENCE   338 AA;  37324 MW;  0B76AFDD68A39BB6 CRC64;

  Query Match           51.3%;  Score 926.5;  DB 1;  Length 338;
  Best Local Similarity   55.1%;  Pred. No. 4.2e-66;
  Matches  179;  Conservative   60;  Mismatches   81;  Indels    5;  Gaps    4;

Qy         20 LAALCLF-QGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTILYAG 78
              |  |||   |:|||| |  | :  ||:||||::| ||| :::: ::|||||| |::||
Db         17 LRLLCLLPTGLPVRSVD--FNRGTDNITVRQGDTAILRCVVEDKNSKVAWLNRSGIIFAG 74

Qy         79 NDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKI 138
              :||| ||||| |      :||: || ||||||| ||||||| : ||||:|:||||| |||
Db         75 HDKWSLDPRVELEKRHALEYSLRIQKVDVYDEGSYTCSVQTQHEPKTSQVYLIVQVPPKI 134

Qy        139 VEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEIQGITREQSGD 198
              ||||:::|||:|::| |:| ||||| :||||::|    |  |:||||| ||||||||
Db        135 SNISSDVTVNEGSNVTLVCMANGRPEPVITWRHLTPLGREFEGEEEYLEILGITREQSGK 194

Qy        199 YECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWYKD 258
              ||| |:|:|::  |::|||||||| |:|:|      |:: :|:|||||||: :|:||:|
Db        195 YECKAANEVSSADVKQVKVTVNYPPTITESKSNEATTGRQASLKCEASAVPAPDFEWYRD 254

Qy        259 DKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIMLFGPGAVSE 318
              | | |   |::::    | |   ||:|  |||||||:|||| ||||::|| ||:|
Db        255 DTR-INSANGLEIKSTEGQSSLTVTNVTEEHYGNYTCVAANKLGVTNASLVLFRPGSVRG 313

Qy        319 VSNGTSRRAGCVWLLPLLVLHLLLK 343
              : ||:   |  :|||  :  || |
Db        314 I-NGSISLAVPLWLLAASLFCLLSK 337
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RESULT 12
KILO_RAT
ID   KILO_RAT       STANDARD;      PRT;   348 AA.
AC   Q9Z0J8;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Kilon protein precursor (Kindred of IgLON).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 32-62.
RX   MEDLINE=99175207; PubMed=10075727;
RA   Funatsu N., Miyata S., Kumanogoh H., Shigeta M., Hamada K., Endo Y.,
RA   Sokawa Y., Maekawa S.;
RT   "Characterization of a novel rat brain glycosylphosphatidylinositol-
RT   anchored protein (Kilon), a member of the IgLON cell adhesion molecule
RT   family.";
RL   J. Biol. Chem. 274:8224-8230(1999).
CC   -!- FUNCTION: CELL-ADHESION (POTENTIAL).
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC   -!- TISSUE SPECIFICITY: Highly expressed in brain.
CC   -!- PTM: GLYCOSYLATED.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
CC       SUBFAMILY.
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB017139; BAA75649.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00408; IGc2; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
KW   Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
KW   Repeat; Signal.
FT   SIGNAL        1     31
FT   CHAIN        32      ?       KILON PROTEIN.
FT   PROPEP        ?    348       REMOVED IN MATURE FORM (POTENTIAL).
FT   DOMAIN       32    128       IG-LIKE C2-TYPE 1.
FT   DOMAIN      133    215       IG-LIKE C2-TYPE 2.
FT   DOMAIN      219    307       IG-LIKE C2-TYPE 3.
FT   DISULFID     54    112       POTENTIAL.
FT   DISULFID    154    197       POTENTIAL.
FT   DISULFID    239    291       POTENTIAL.
FT   CARBOHYD     67     67       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    149    149       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    269    269       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    280    280       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    288    288       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    301    301       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   348 AA;  37858 MW;  37E90D1C7D24ACAB CRC64;

  Query Match           45.1%;  Score 815;  DB 1;  Length 348;
  Best Local Similarity   47.5%;  Pred. No. 2.9e-57;
  Matches  160;  Conservative   66;  Mismatches  101;  Indels   10;  Gaps    5;

Qy         11 SISW--AIFTGLAALCLFQGVPVRSGDATFP-KAMDNVTVRQGESATLRCTIDNRVTRVA 67
              |  |  |:  | : ||  |  |      ||  |:||: ||:|::| ||| :::  :: |
Db         11 SNQWLAAVLLSLCS-CLPAGQSV-----DFPWAAVDNMLVRKGDTAVLRCYLEDGASKGA 64
```

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                ||| |:|:||:  |::|:|||||||| |:|:|      |::  |:||||||||: :|:||:|
Db        195 YECKAANEVASADVKQVRVTVNYPPTITESKSNEAATGRQALLRCEASAVPTPDFEWYRD 254

Qy        259 DKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIMLFGPGAVSE 318
              | |.|    |:::::    | |:  ||:|  ||||||||:|||| ||||: |: ||
Db        255 DTR-INSANGLEIKSTGSQSLLMVANVTEEHYGNYTCVAANKLGVTNASLYLYRPG-TGR 312

Qy        319 VSNGTSRRAGCVWLLPLLVLHLLLK 343
              | ||:   |  :|||  :| || |
Db        313 VDNGSVSLAVPLWLLAASLLCLLSK 337


RESULT 10
LAMP_HUMAN
ID   LAMP_HUMAN     STANDARD;      PRT;   338 AA.
AC   Q13449;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Limbic system-associated membrane protein precursor (LSAMP).
GN   LSAMP OR LAMP.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96235133; PubMed=8666243;
RA   Pimenta A.F., Fischer I., Levitt P.;
RT   "cDNA cloning and structural analysis of the human limbic-system-
RT   associated membrane protein (LAMP).";
RL   Gene 170:189-195(1996).
CC   -!- FUNCTION: MEDIATES SELECTIVE NEURONAL GROWTH AND AXON TARGETING.
CC       CONTRIBUTES TO THE GUIDANCE OF DEVELOPING AXONS AND REMODELING OF
CC       MATURE CIRCUITS IN THE LIMBIC SYSTEM. ESSENTIAL FOR NORMAL GROWTH
CC       OF THE HYPPOCAMPAL MOSSY FIBER PROJECTION (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC   -!- TISSUE SPECIFICITY: EXPRESSED ON LIMBIC NEURONS AND FIBER TRACTS
CC       AS WELL AS IN SINGLE LAYERS OF THE SUPERIOR COLLICULUS, SPINAL
CC       CHORD AND CEREBELLUM.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
CC       SUBFAMILY.
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U41901; AAC50569.1; -.
DR   PIR; JC4776; JC4776.
DR   Genew; HGNC:6705; LSAMP.
DR   MIM; 603241; -.
DR   GO; GO:0007399; P:neurogenesis; TAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00408; IGc2; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
KW   Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
KW   Repeat; Signal.
FT   SIGNAL      1     28       POTENTIAL.
FT   CHAIN       29    315      LIMBIC SYSTEM-ASSOCIATED MEMBRANE
FT                              PROTEIN.
FT   PROPEP      316   338      REMOVED IN MATURE FORM (POTENTIAL).
FT   DOMAIN      29    122      IG-LIKE C2-TYPE 1.
FT   DOMAIN      132   214      IG-LIKE C2-TYPE 2.
FT   DOMAIN      219   304      IG-LIKE C2-TYPE 3.
FT   DISULFID    53    111      POTENTIAL.
FT   DISULFID    153   197      POTENTIAL.
FT   DISULFID    239   290      POTENTIAL.
FT   CARBOHYD    40    40       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    66    66       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    136   136      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    148   148      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    279   279      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    287   287      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    300   300      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    315   315      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   LIPID       315   315      GPI-ANCHOR (POTENTIAL).
SQ   SEQUENCE   338 AA;  37308 MW;  03455F286DF5D92F CRC64;

 Query Match           51.6%;  Score 931.5;  DB 1;  Length 338;
 Best Local Similarity 55.4%;  Pred. No. 1.7e-66;
 Matches  180;  Conservative   60;  Mismatches   80;  Indels    5;  Gaps    4;

Qy         20 LAALCLF-QGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTILYAG 78
              |  |||   |:|||| |  | :.||:||||::| ||| :::: ::|||||| |::||
Db         17 LRLLCLLPTGLPVRSVD--FNRGTDNITVRQGDTAILRCVLEDKNSKVAWLNRSGIIFAG 74

Qy         79 NDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKI 138
              :||| ||||| |      :||: || ||||||| |||||||  : ||||:|:||||| |||
Db         75 HDKWSLDPRVELEKRHSLEYSLRIQKVDVYDEGSYTCSVQTQHEPKTSQVYLIVQVPPKI 134

Qy        139 VEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEIQGITREQSGD 198
                |||:::|||:|::| |:| ||||| :||||::|    |  |:|||| ||||||||
Db        135 SNISSDVTVNEGSNVTLVCMANGRPEPVITWRHLTPTGREFEGEEEYLEILGITREQSGK 194

Qy        199 YECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWYKD 258
              ||| |:|:|::  |::|||||||| |:|:|    |:: :|:|||||||: :|:||:|
Db        195 YECKAANEVSSADVKQVKVTVNYPPTITESKSNEATTGRQASLKCEASAVPAPDFEWYRD 254

Qy        259 DKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIMLFGPGAVSE 318
              | | |    |:::::    | |   ||:|  ||||||||:|||| ||||::|| ||:|
Db        255 DTR-INSANGLEIKSTEGQSSLTVTNVTEEHYGNYTCVAANKLGVTNASLVLFRPGSVRG 313

Qy        319 VSNGTSRRAGCVWLLPLLVLHLLLK 343
              : ||:   |  :|||   :| || |
Db        314 I-NGSISLAVPLWLLAASLLCLLSK 337


RESULT 11
LAMP_RAT
ID   LAMP_RAT       STANDARD;      PRT;   338 AA.
AC   Q62813;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Limbic system-associated membrane protein precursor (LSAMP).
GN   LSAMP OR LAMP.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 29-49.
RC   TISSUE=Hippocampus;
RX   MEDLINE=95374785; PubMed=7646886;
RA   Pimenta A.F., Zhukareva V., Barbe M.F., Reinoso B.S., Grimley C.,
RA   Henzel W., Fischer I., Levitt P.;
RT   "The limbic system-associated membrane protein is an Ig superfamily
RT   member that mediates selective neuronal growth and axon targeting.";
RL   Neuron 15:287-297(1995).
CC   -!- FUNCTION: MEDIATES SELECTIVE NEURONAL GROWTH AND AXON TARGETING.
CC       CONTRIBUTES TO THE GUIDANCE OF DEVELOPING AXONS AND REMODELING OF
CC       MATURE CIRCUITS IN THE LIMBIC SYSTEM. ESSENTIAL FOR NORMAL GROWTH
CC       OF THE HYPPOCAMPAL MOSSY FIBER PROJECTION.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC   -!- TISSUE SPECIFICITY: EXPRESSED MOSTLY BY NEURONS COMPRISING LIMBIC-
CC       ASSOCIATED CORTICAL AND SUBCORTICAL REGIONS THAT FUNCTION IN
CC       COGNITION, EMOTION, MEMORY, AND LEARNING.
CC   -!- DEVELOPMENTAL STAGE: FIRST DETECTED AT E15-16, AT STAGE E20 IT IS
```

```
FT   SIGNAL       1    27       BY SIMILARITY.
FT   CHAIN       28   322       OPIOID BINDING PROTEIN/CELL ADHESION
FT                              MOLECULE.
FT   PROPEP     323   345       REMOVED IN MATURE FORM (POTENTIAL).
FT   DOMAIN      39   126       IG-LIKE C2-TYPE 1.
FT   DOMAIN     136   219       IG-LIKE C2-TYPE 2.
FT   DOMAIN     223   310       IG-LIKE C2-TYPE 3.
FT   DISULFID    57   115       POTENTIAL.
FT   DISULFID   157   202       POTENTIAL.
FT   DISULFID   244   296       POTENTIAL.
FT   CARBOHYD    44    44       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    70    70       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   140   140       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   285   285       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   293   293       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   306   306       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   LIPID      322   322       GPI-ANCHOR (POTENTIAL).
FT   VARSPLIC     1    27       MGVCGYLFLPWKCLVVVSLRLLFLVPT -> MYHPAYWIVF
FT                              SATTALLFIP (in isoform 2).
FT                              /FTId=VSP_002612.
SQ   SEQUENCE   345 AA;  38067 MW;  A3181B0753F9658E CRC64;

  Query Match             69.7%;  Score 1259;  DB 1;  Length 345;
  Best Local Similarity   71.2%;  Pred. No. 2.1e-92;
  Matches  240;  Conservative   34;  Mismatches   59;  Indels    4;  Gaps    2;

Qy         12 ISWAIFTGLAALCLF---QGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAW 68
              : |     ::   ||    ||||||||||||||||||||||||||||||:|||||||
Db          9 LPWKCLVVVSLRLLFLVPTGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDDRVTRVAW 68

Qy         69 LNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRV 128
              |||||||||||||| :||||::| || ||||| ||||||||||||||||||||||||||
Db         69 LNRSTILYAGNDKWSIDPRVIILVNTPTQYSIMIQNVDVYDEGPYTCSVQTDNHPKTSRV 128

Qy        129 HLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPK-AVGFVSEDEYLE 187
              |||||| |:|: |||||::|| ::::| |:| ||||||||||:| |   ||||||||||
Db        129 HLIVQVPPQIMNISSDITVNEISSVTLLCLAIGRPEPTVTWRHLSVKEGQGFVSEDEYLE 188

Qy        188 IQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASA 247
              |  | |:|||:||||| |||||| ||:||:|||||||||:|| ||| ||||| | |||||
Db        189 ISDIKRDQSGEYECSALNDVAAPDVRKVKITVNYPPYISKAKNTGVSVGQKGILSCEASA 248

Qy        248 VPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNAS 307
              || |||||:|:| ||  |  ||::||:  :| | |||||| ||||||||:||||:||||
Db        249 VPMAEFQWFKEDTRLATGLDGVRIENKGRISTLTFFNVSEKDYGNYTCVATNKLGNTNAS 308

Qy        308 IMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
              | |:|||| :  |  ||   |:||     |  :||
Db        309 ITLYGPGAVIDGVNSASRALACLWLSGTFFAHFFIKF 345


RESULT 9
LAMP_CHICK
ID   LAMP_CHICK     STANDARD;      PRT;   338 AA.
AC   Q98919;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Limbic system-associated membrane protein precursor (E19S) (CHLAMP,
DE   G19-isoform).
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=97157768; PubMed=9004047;
RA   Wilson D.J.A., Kim D.S., Clarke G.A., Marshall-Clarke S., Moss D.J.;
RT   "A family of glycoproteins (GP55), which inhibit neurite outgrowth,
RT   are members of the Ig superfamily and are related to OBCAM,
RT   neurotrimin, LAMP and CEPU-1.";
RL   J. Cell Sci. 109:3129-3138(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=97358596; PubMed=9215692;
RA   Brummendorf T., Spaltmann F., Treubert U.;
RT   "Cloning and characterization of a neural cell recognition molecule
RT   on axons of the retinotectal system and spinal cord.";
RL   Eur. J. Neurosci. 9:1105-1116(1997).
CC   -!- FUNCTION: MEDIATES SELECTIVE NEURONAL GROWTH AND AXON TARGETING.
CC       PROBABLY SERVES AS A RECOGNITION MOLECULE FOR THE FORMATION OF
CC       LIMBIC CONNECTIONS (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC       similarity).
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
CC       SUBFAMILY.
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y08171; CAA69357.1; -.
DR   EMBL; Z94720; CAB08115.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00408; IGc2; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
KW   Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
KW   Repeat; Signal.
FT   SIGNAL       1    28       POTENTIAL.
FT   CHAIN       29   338       LIMBIC SYSTEM-ASSOCIATED MEMBRANE
FT                              PROTEIN.
FT   PROPEP      29   338       REMOVED IN MATURE FORM (POTENTIAL).
FT   DOMAIN      29   122       IG-LIKE C2-TYPE 1.
FT   DOMAIN     132   214       IG-LIKE C2-TYPE 2.
FT   DOMAIN     219   306       IG-LIKE C2-TYPE 3.
FT   DISULFID    53   111       POTENTIAL.
FT   DISULFID   153   197       POTENTIAL.
FT   DISULFID   239   290       POTENTIAL.
FT   CARBOHYD    40    40       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    66    66       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   136   136       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   148   148       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   279   279       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   287   287       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   300   300       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   315   315       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   338 AA;  37394 MW;  8FA4A60AD98426B4 CRC64;

  Query Match             52.0%;  Score 938.5;  DB 1;  Length 338;
  Best Local Similarity   56.0%;  Pred. No. 4.7e-67;
  Matches  182;  Conservative   56;  Mismatches   82;  Indels    5;  Gaps    4;

Qy         20 LAALCLF-QGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTILYAG 78
              |  |||   |:|||| |  | :  ||:|||||::| ||| :::| ::|||||| |::||
Db         17 LRLLCLLPTGLPVRSVD--FTRGTDNITVRQGDTAILRCFVEDRSSKVAWLNRSGIIFAG 74

Qy         79 NDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKI 138
               ||| ||||| |   :  :||: || ||||||| ||||||| :|||||:|:||||| |||
Db         75 EDKWSLDPRVELEKRSPLEYSLRIQKVDVYDEGSYTCSVQTQHHPKTSQVYLIVQVPPKI 134

Qy        139 VEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEIQGITREQSGD 198
              |||||:|||:|::| |:| ||||| :||||::|    |  |:||||| ||||||||
Db        135 SNISSDITVNEGSNVTLVCMANGRPEPVITWRHLTPTGKEFEGEEEYLEILGITREQSGK 194

Qy        199 YECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWYKD 258
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RX   MEDLINE=89251576; PubMed=2721489;
RA   Schofield P.R., McFarland K.C., Hayflick J.S., Wilcox J.N.,
RA   Cho T.M., Roy S., Lee N.M., Loh H.H., Seeburg P.H.;
RT   "Molecular characterization of a new immunoglobulin superfamily
RT   protein with potential roles in opioid binding and cell contact.";
RL   EMBO J. 8:489-495(1989).
CC   -!- FUNCTION: Binds opioids in the presence of acidic lipids; probably
CC       involved in cell contact.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC       similarity).
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
CC       SUBFAMILY.
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X12672; CAA31192.1; -.
DR   PIR; S03199; S03199.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00408; IGc2; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
KW   Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
KW   Repeat; Signal.
FT   SIGNAL       1     27
FT   CHAIN       28    322       OPIOID BINDING PROTEIN/CELL ADHESION
FT                                 MOLECULE.
FT   PROPEP      323    345       REMOVED IN MATURE FORM (POTENTIAL).
FT   DOMAIN       39    126       IG-LIKE C2-TYPE 1.
FT   DOMAIN      136    219       IG-LIKE C2-TYPE 2.
FT   DOMAIN      223    310       IG-LIKE C2-TYPE 3.
FT   DISULFID     57    115       POTENTIAL.
FT   DISULFID    157    202       POTENTIAL.
FT   DISULFID    244    296       POTENTIAL.
FT   CARBOHYD     44     44       N-LINKED (GLCNAC. . .) (PROBABLE).
FT   CARBOHYD     70     70       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    140    140       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    285    285       N-LINKED (GLCNAC. . .) (PROBABLE).
FT   CARBOHYD    293    293       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    306    306       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   LIPID       322    322       GPI-ANCHOR (POTENTIAL).
SQ   SEQUENCE   345 AA;  37914 MW;  D1ECC8D9E7D8CB19 CRC64;

  Query Match          70.1%;  Score 1266;  DB 1;  Length 345;
  Best Local Similarity  71.6%;  Pred. No. 5.9e-93;
  Matches  240;  Conservative   34;  Mismatches   57;  Indels    4;  Gaps    2;

Qy         14 WAIFTGLAALCLF---QGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLN 70
              |     ::   ||    ||||||||||||||||||||||||||||||||:|||||||||
Db         11 WKCLVVVSLRLLFLVPTGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDDRVTRVAWLN 70

Qy         71 RSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRVHL 130
              |||||||||||| :||||::| || ||||| ||||||||||||||||||||||||||||
Db         71 RSTILYAGNDKWSIDPRVIILVNTPTQYSIMIQNVDVYDEGPYTCSVQTDNHPKTSRVHL 130

Qy        131 IVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPK-AVGFVSEDEYLEIQ 189
              |||| |:|: ||||:::|||::::| |:| ||||||||||:| |   ||||||||||
Db        131 IVQVPPQIMNISSDVTVNEGSSVTLLCLAIGRPEPTVTWRHLSVKEGQGFVSEDEYLEIS 190

Qy        190 GITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVP 249
               | |:|||:|||| |||||| ||:||:|||||||||:|| ||| ||||| | |||||||
Db        191 DIKRDQSGEYECSALNDVAAPDVRKVKITVNYPPYISKAKNTGVSVGQKGILSCEASAVP 250

Qy        250 SAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIM 309
              |||||:|:| ||  |  |::::||: :| | |||||| ||||||||:|||| |||||
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Db        251 MAEFQWFKEDTRLATGLDGMRIENKGHISTLTFFNVSEKDYGNYTCVATNKLGITNASIT 310

Qy        310 LFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
              |:|||| : ||  ||   |:||   | |  :||
Db        311 LYGPGAVIDGVNSASRALACLWLSGTLFAHFFIKF 345


RESULT 8
OPCM_RAT
ID   OPCM_RAT       STANDARD;      PRT;   345 AA.
AC   P32736; P32735; Q01653; Q01654;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Opioid binding protein/cell adhesion molecule precursor (OBCAM)
DE   (Opioid-binding cell adhesion molecule) (OPCML).
GN   OPCML OR OBCAM.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92347701; PubMed=1339369;
RA   Lippman D.A., Lee N.M., Loh H.H.;
RT   "Opioid-binding cell adhesion molecule (OBCAM)-related clones from a
RT   rat brain cDNA library.";
RL   Gene 117:249-254(1992).
RN   [2]
RP   SEQUENCE OF 195-214, AND GPI-ANCHOR.
RX   MEDLINE=95198094; PubMed=7891157;
RA   Struyk A.F., Canoll P.D., Wolfgang M.J., Rosen C.L., D'Eustachio P.,
RA   Salzer J.L.;
RT   "Cloning of neurotrimin defines a new subfamily of differentially
RT   expressed neural cell adhesion molecules.";
RL   J. Neurosci. 15:2141-2156(1995).
CC   -!- FUNCTION: Binds opioids in the presence of acidic lipids; probably
CC       involved in cell contact.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms seem to exist;
CC       Name=1;
CC         IsoId=P32736-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=P32736-2; Sequence=VSP_002612;
CC         Note=No experimental confirmation available;
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
CC       SUBFAMILY.
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M88710; AAA40859.1; -.
DR   EMBL; M88711; AAA40860.1; -.
DR   EMBL; M88709; AAA40858.1; -.
DR   PIR; JC1238; JC1238.
DR   PIR; JC1239; JC1239.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00408; IGc2; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
KW   Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
KW   Repeat; Signal; Alternative splicing.
```

```
Qy          8 MHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVA 67
              |::   |:::|   ||    ||||||||||||||||||||||||||||||:|:|| |||
Db          1 MYHPACWIVFTATTALLFIPGVPVRSGDATFPKAMDNVTVRQGESATLRCTVDDRVRRVA 60

Qy         68 WLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSR 127
              |||||||||||||||| :| |||:||||:|||||:| ||||||||||||||||||||||||
Db         61 WLNRSTILYAGNDKWSIDNRVVILSNTKTQYSIKIHNVDVYDEGPYTCSVQTDNHPKTSR 120

Qy        128 VHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLE 187
              ||||||| |:|| |||||::|||:::::| |:| ||||||||||:| |  ||||||||||
Db        121 VHLIVQVPPQIVNISSDITVNEGSSVTLMCLAFGRPEPTVTWRHLSGKGQGFVSEDEYLE 180

Qy        188 IQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASA 247
              | |||||||:||||| |||| |:||:||||||||||| || ||  ||||| ||||||||
Db        181 ITGITREQSGEYECSAVNDVAVPDVRKVKVTVNYPPYISNAKNTGASVGQKGILQCEASA 240

Qy        248 VPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNAS 307
              || |||||:|:| ||  | :||::|::  || | |||||| |||||||||:||||:||||
Db        241 VPVAEFQWFKEDTRLANGLEGVRIESKGRLSTLTFFNVSEKDYGNYTCVATNKLGNTNAS 300

Qy        308 IMLFGPGAVSEVSNGTSRRAG--CVWLLPLLVLHLLLKF 344
              |:|:|||||  :  |  || |   |:|     |:  ||| |
Db        301 IILYGPGAVHDSGNAASRAAAGLCLW--ATLLARLLLDF 337


RESULT 6
OPCM_HUMAN
ID   OPCM_HUMAN     STANDARD;      PRT;   345 AA.
AC   Q14982;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Opioid binding protein/cell adhesion molecule precursor (OBCAM)
DE   (Opioid-binding cell adhesion molecule) (OPCML).
GN   OPCML OR OBCAM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Occipital cortex;
RX   MEDLINE=95237612; PubMed=7721093;
RA   Shark K.B., Lee N.M.;
RT   "Cloning, sequencing and localization to chromosome 11 of a cDNA
RT   encoding a human opioid-binding cell adhesion molecule (OBCAM).";
RL   Gene 155:213-217(1995).
CC   -!- FUNCTION: Binds opioids in the presence of acidic lipids; probably
CC       involved in cell contact.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC       similarity).
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
CC       SUBFAMILY.
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L34774; AAA36387.1; -.
DR   PIR; JC4025; JC4025.
DR   Genew; HGNC:8143; OPCML.
DR   MIM; 600632; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0004985; F:opioid receptor activity; TAS.
DR   GO; GO:0007155; P:cell adhesion; TAS.
DR   GO; GO:0008038; P:neuronal cell recognition; TAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00408; IGc2; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
KW   Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
KW   Repeat; Signal.
FT   SIGNAL       1     27       BY SIMILARITY.
FT   CHAIN       28    322       OPIOID BINDING PROTEIN/CELL ADHESION
FT                               MOLECULE.
FT   PROPEP     323    345       REMOVED IN MATURE FORM (POTENTIAL).
FT   DOMAIN      39    126       IG-LIKE C2-TYPE 1.
FT   DOMAIN     136    219       IG-LIKE C2-TYPE 2.
FT   DOMAIN     223    310       IG-LIKE C2-TYPE 3.
FT   DISULFID    57    115       POTENTIAL.
FT   DISULFID   157    202       POTENTIAL.
FT   DISULFID   244    296       POTENTIAL.
FT   CARBOHYD    44     44       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    70     70       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   140    140       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   285    285       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   293    293       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   306    306       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   LIPID      322    322       GPI-ANCHOR (POTENTIAL).
SQ   SEQUENCE   345 AA;  38007 MW;  E7AD17BEA1AA3FF4 CRC64;

  Query Match             70.2%;  Score 1268;  DB 1;  Length 345;
  Best Local Similarity   71.2%;  Pred. No. 4.1e-93;
  Matches  240;  Conservative   37;  Mismatches   56;  Indels    4;  Gaps    2;

Qy         12 ISWAIFTGLAALCLF---QGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAW 68
              : |     ::   ||   ||||||||||||||||||||||||||||||:|||||||
Db          9 LPWKCLVVVSLRLLFLVPTGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDDRVTRVAW 68

Qy         69 LNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRV 128
              |||||||||||||| :|||||:| || ||||| |||||||||||||||||||||||||||
Db         69 LNRSTILYAGNDKWSIDPRVIILVNTPTQYSIMIQNVDVYDEGPYTCSVQTDNHPKTSRV 128

Qy        129 HLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPK-AVGFVSEDEYLE 187
              |||||| |:|: |||||::|||:::::| |:| ||||||||||:| |   ||||||||||
Db        129 HLIVQVPPQIMNISSDITVNEGSSVTLLCLAIGRPEPTVTWRHLSVKEGQGFVSEDEYLE 188

Qy        188 IQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASA 247
              |  | |:|||:||||| |||||| ||:||:|||||||||:|| ||| ||||| | |||||
Db        189 ISDIKRDQSGEYECSALNDVAAPDVRKVKITVNYPPYISKAKNTGVSVGQKGILSCEASA 248

Qy        248 VPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNAS 307
              || |||||:|:: ||  |  |:::||:  :| | ||||||  ||||||||:||||:||||
Db        249 VPMAEFQWFKEETRLATGLDGMRIENKGRMSTLTFFNVSEKDYGNYTCVATNKLGNTNAS 308

Qy        308 IMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
              | |:|||||  :  |  ||   |:||   |: |  :||
Db        309 ITLYGPGAVIDGVNSASRALACLWLSGTLLAHFFIKF 345


RESULT 7
OPCM_BOVIN
ID   OPCM_BOVIN     STANDARD;      PRT;   345 AA.
AC   P11834;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-OCT-1989 (Rel. 12, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Opioid binding protein/cell adhesion molecule precursor (OBCAM)
DE   (Opioid-binding cell adhesion molecule) (OPCML).
GN   OPCML OR OBCAM OR OCAM.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   TISSUE=Brain;
```

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                    N COINCIDES WITH THE GROWTH OF THE DENDRITIC TREE,
                    CELLS HAVE FINISHED THEIR MIGRATION FROM THE
                    ZONE (FROM E15 UNTIL E21). EXPRESSED IN THE ADULT.
                    Y: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
                    ILY.
                    LARITY: Contains 3 immunoglobulin-like C2-type domains.
                    ----------------------------------------------------------------------
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                    between the Swiss Institute of Bioinformatics and the EMBL outstation -
                    the European Bioinformatics Institute. There are no restrictions on its
CC                  use by non-profit institutions as long as its content is in no way
CC                  modified and this statement is not removed. Usage by and for commercial
CC                  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC                  or send an email to license@isb-sib.ch).
CC                  ----------------------------------------------------------------------
DR                  EMBL; Z72497; CAA96578.1; -.
DR                  InterPro; IPR007110; Ig-like.
DR                  InterPro; IPR003598; Ig_c2.
DR                  InterPro; IPR003006; Ig_MHC.
DR                  Pfam; PF00047; ig; 3.
DR                  SMART; SM00408; IGc2; 2.
DR                  PROSITE; PS50835; IG_LIKE; 3.
KW                  Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
KW                  Repeat; Signal; Alternative splicing.
FT                  SIGNAL       1     28       POTENTIAL.
FT                  CHAIN       29    330       CEPU-1 PROTEIN.
FT                  PROPEP     331    353       REMOVED IN MATURE FORM (POTENTIAL).
FT                  DOMAIN      37    124       IG-LIKE C2-TYPE 1.
FT                  DOMAIN     134    216       IG-LIKE C2-TYPE 2.
FT                  DOMAIN     220    314       IG-LIKE C2-TYPE 3.
FT                  DISULFID    55    113       POTENTIAL.
FT                  DISULFID   155    199       POTENTIAL.
FT                  DISULFID   241    293       POTENTIAL.
FT                  CARBOHYD    42     42       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT                  CARBOHYD    68     68       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT                  CARBOHYD   150    150       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT                  CARBOHYD   282    282       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT                  CARBOHYD   290    290       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT                  CARBOHYD   303    303       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT                  LIPID      330    330       GPI-ANCHOR (POTENTIAL).
FT                  VARSPLIC   310    320       Missing (in isoform 2).
FT                                              /FTId=VSP_002607.
SQ                  SEQUENCE   353 AA;  38736 MW;  2550C48591EBBBA6 CRC64;

  Query Match             81.8%;  Score 1477.5;  DB 1;  Length 353;
  Best Local Similarity   78.6%;  Pred. No. 1.1e-109;
  Matches  276;  Conservative   32;  Mismatches   32;  Indels   11;  Gaps    1;

Qy          5 QPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVT 64
              | ||. : :|| || |:||| |||||||||||||||||||||||||||||::|||||
Db          3 QAKMQHPVSWVIFAGMAALLLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCSVDNRVT 62

Qy         65 RVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPK 124
              ||||||||:|||||||||||||||||:||:|||||:| :|||||||||||||||||||
Db         63 RVAWLNRSSILYAGNDKWCLDPRVVLLANTKTQYSIQIHDVDVYDEGPYTCSVQTDNHPK 122

Qy        125 TSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDE 184
              |||||||||||||| | ||||||||| |:|||||||||:||:||||||||||||:||||
Db        123 TSRVHLIVQVSPKITETSSDISINEGGNVSLTCIATGRPDPTITWRHISPKAVGFISEDE 182

Qy        185 YLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCE 244
              |||| |||||||:|||||||||||||||:|||||||||||||:|| |||||||| | ||
Db        183 YLEITGITREQSGEYECSASNDVAAPVVQRVKVTVNYPPYISDAKSTGVPVGQKGILMCE 242

Qy        245 ASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHT 304
              |||||||:|||||||||| ||:||:|||| | |:| |||||| ||||||||||:||:|
Db        243 ASAVPSADFQWYKDDKRLAEGQKGLKVENKAFFSRLTFFNVSEQDYGNYTCVASNQLGNT 302

Qy        305 NASIMLF----------GPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
              |||::|:          ||||| : ::|  ||  | ||| | :  |  :|
Db        303 NASMILYEETTTALTPWKGPGAVHDGNSGAWRRGSCAWLLALPLAQLARQF 353
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RESULT 5
G55A_CHICK
ID   G55A_CHICK     STANDARD;      PRT;   337 AA.
AC   Q98892;
DT   01-NOV-1997 (Rel. 35, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Neurite inhibitor GP55-A precursor (OBCAM protein gamma
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; i        ..ae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Lodge A.P., Kim D.-S., Howard M.R., McNamee C.J., Smith N., Moss D.J.;
RT   "Cloning of CEPU-s, a secreted isoform of CEPU-1, and OBCAM cDNAs from
RT   chick: structural diversity of IgLON family proteins.";
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 64-337 FROM N.A., AND PARTIAL SEQUENCE.
RC   TISSUE=Brain;
RX   MEDLINE=97157768; PubMed=9004047;
RA   Wilson D.J.A., Kim D.-S., Clarke G.A., Marshall-Clarke S., Moss D.J.;
RT   "A family of glycoproteins (GP55), which inhibit neurite outgrowth,
RT   are members of the Ig superfamily and are related to OBCAM,
RT   neurotrimin, LAMP and CEPU-1.";
RL   J. Cell Sci. 109:3129-3138(1996).
CC   -!- FUNCTION: INHIBITS NEURITE OUTGROWTH.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC   -!- TISSUE SPECIFICITY: RESTRICTED TO THE NERVOUS SYSTEM.
CC   -!- DEVELOPMENTAL STAGE: INCREASES DURING DEVELOPMENT FROM VERY LOW
CC       LEVELS AT EMBRYONIC DAY 10 AND IS MOST ABUNDANT AFTER HATCHING.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
CC       SUBFAMILY.
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; Y08170; CAB41420.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00408; IGc2; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
KW   Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
KW   Repeat; Signal.
FT   SIGNAL       1     20       BY SIMILARITY.
FT   CHAIN       21    317       NEURITE INHIBITOR GP55-A (POTENTIAL).
FT   PROPEP     318    337       REMOVED IN MATURE FORM (POTENTIAL).
FT   DOMAIN      32    119       IG-LIKE C2-TYPE 1.
FT   DOMAIN     129    211       IG-LIKE C2-TYPE 2.
FT   DOMAIN     215    302       IG-LIKE C2-TYPE 3.
FT   DISULFID    50    108       POTENTIAL.
FT   DISULFID   150    194       POTENTIAL.
FT   DISULFID   236    288       POTENTIAL.
FT   CARBOHYD   133    133       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   277    277       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   285    285       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   298    298       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   337 AA;  36887 MW;  BAE7175518566516 CRC64;

  Query Match             72.3%;  Score 1305;  DB 1;  Length 337;
  Best Local Similarity   73.2%;  Pred. No. 4.7e-96;
  Matches  248;  Conservative   34;  Mismatches   53;  Indels    4;  Gaps    2;
```

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Db        189 QGITREQSGEYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAV 248

Qy        249 PSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASI 308
              ||||||:||||||:||||||||||||||| ||||||||||||||||||||||||||||||
Db        249 PSAEFQWFKDDKRLVEGKKGVKVENRPFLSKLTFFNVSEHDYGNYTCVASNKLGHTNASI 308

Qy        309 MLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
              ||||||||||:|||||||||:|||||||||||||||
Db        309 MLFGPGAVSEVNNGTSRRAGCIWLLPLLVLHLLLKF 344

RESULT 3
NTRI_RAT
ID   NTRI_RAT       STANDARD;      PRT;   344 AA.
AC   Q62718;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Neurotrimin precursor (GP65).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 217-229.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=95198094; PubMed=7891157;
RA   Struyk A.F., Canoll P.D., Wolfgang M.J., Rosen C.L., D'Eustachio P.,
RA   Salzer J.L.;
RT   "Cloning of neurotrimin defines a new subfamily of differentially
RT   expressed neural cell adhesion molecules.";
RL   J. Neurosci. 15:2141-2156(1995).
CC   -!- FUNCTION: Neural cell adhesion molecule.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC   -!- TISSUE SPECIFICITY: CENTRAL NERVOUS SYSTEM.
CC   -!- DEVELOPMENTAL STAGE: EXPRESSED AT HIGH LEVELS IN SEVERAL
CC       DEVELOPING PROJECTION SYSTEMS: IN NEURONS OF THE THALAMUS,
CC       SUBPLATE, AND LOWER CORTICAL LAMINAE IN THE FOREBRAIN AND IN THE
CC       PONTINE NUCLEUS, CEREBELLAR GRANULE CELLS, AND PURKINJE CELLS IN
CC       THE HINDBRAIN.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
CC       SUBFAMILY.
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this st- -ment is not removed. Usage by and for commercial
CC   entities require-      -nse agreement (See http://www.isb-sib.ch/announce/
CC   or send an e-          -se@isb-sib.ch).
CC   --------               ---------------------------------------------------
DR   EMBL-
DR   D-
DP                 e.

CC
CC
CC
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CC
CC
     CELLS. EXPRESSIO-
     AFTER PURKINJE
     VENTRICULAR
     -!- SIMILARIT-
     SUBFAM-
     -!- SIM-
     -----
     Th-

                   -sion; Glycoprotein; GPI-anchor;

                   -TIAL.
                    TRIMIN.
                   -D IN MATURE FORM (POTENTIAL).
                    C2-TYPE 1.
                    C2-TYPE 2.
                    C2-TYPE 3.

                         LCNAC. . .) (POTENTIAL).
                          CNAC. . .) (POTENTIAL).

Thu Sep 11 16:21:00 2003

FT   CARBOHYD    152    152       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    216    216       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    284    284       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    292    292       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    305    305       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    321    321       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   LIPID       321    321       GPI-ANCHOR (POTENTIAL).
SQ   SEQUENCE   344 AA;  37998 MW;  CBB39BE53B33B224 CRC64;

  Query Match            90.8%;  Score 1639.5;  DB 1;  Length 344;
  Best Local Similarity  92.9%;  Pred. No. 1.6e-122;
  Matches  312;  Conservative    9;  Mismatches   12;  Indels    3;  Gaps    1;

Qy         12 ISWAIFTGLAALCLF---QGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAW 68
              : |     ::   ||   ||||||||||||||||||||||||||||||||||||||||||
Db          9 LPWKCLVVVSLRLLFLVPTGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAW 68

Qy         69 LNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRV 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 LNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRV 128

Qy        129 HLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEI 188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 HLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEI 188

Qy        189 QGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAV 248
              ||||||||:|||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        189 QGITREQSGEYECSASNDVAAPVVRRVNVTVNYPPYISEAKGTGVPVGQKGTLQCEASAV 248

Qy        249 PSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASI 308
              ||||||:||:||:|:|||||||||||||||:|:|||||||||||||||||||||||||||
Db        249 PSAEFQWFKDDKRLVEGKKGVKVENRPFLSRLTFFNVSEHDYGNYTCVASNKLGHTNASI 308

Qy        309 MLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
              ||||||||||:|||||||||:|||||||||||||||
Db        309 MLFGPGAVSEVNNGTSRRAGCIWLLPLLVLHLLLKF 344

RESULT 4
CEPU_CHICK
ID   CEPU_CHICK     STANDARD;      PRT;   353 AA.
AC   Q90773;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   CEPU-1 protein precursor.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC   TISSUE=Brain;
RX   MEDLINE=96370549; PubMed=8774445;
RA   Spaltmann F., Bruemmendorf T.;
RT   "CEPU-1, a novel immunoglobulin superfamily molecule, is expressed by
RT   developing cerebellar Purkinje cells.";
RL   J. Neurosci. 16:1770-1779(1996).
CC   -!- FUNCTION: IT MAY BE A CELLULAR ADDRESS MOLECULE SPECIFIC TO
CC       PURKINJE CELLS. IT MAY REPRESENT A RECEPTOR OR A SUBUNIT OF A
CC       RECEPTOR COMPLEX.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1; Synonyms=Minor;
CC         IsoId=Q90773-1; Sequence=Displayed;
CC       Name=2; Synonyms=Major;
CC         IsoId=Q90773-2; Sequence=VSP_002607;
CC   -!- TISSUE SPECIFICITY: FOUND ON THE DENDRITES, SOMATA AND AXONS -
CC       DEVELOPING PURKINJE CELLS. UNDETECTABLE ON OTHER NEURONS L-
CC       GOLGI OR GRANULE CELLS.
CC   -!- DEVELOPMENTAL STAGE: EXPRESSED BY DEVELOPING CEREBELL-
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FT   CARBOHYD    305    305       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    321    321       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   LIPID       321    321       GPI-ANCHOR (POTENTIAL).
SQ   SEQUENCE   344 AA;  37971 MW;  DA4D12C295ABBE3A CRC64;

  Query Match           92.2%;  Score 1665.5;  DB 1;  Length 344;
  Best Local Similarity   95.2%;  Pred. No. 1.4e-124;
  Matches  320;  Conservative    3;  Mismatches   10;  Indels    3;  Gaps    1;

Qy         12 ISWAIFTGLAALCLF---QGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAW 68
              : |    ::   ||    ||||||||||||||||||||||||||||||||||||||||
Db          9 LPWKCLVVVSLRLLFLVPTGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAW 68

Qy         69 LNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRV 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 LNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRV 128

Qy        129 HLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEI 188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 HLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEI 188

Qy        189 QGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAV 248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 QGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAV 248

Qy        249 PSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASI 308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 PSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASI 308

Qy        309 MLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
              ||||||||||||||||||||||||||||||||||||
Db        309 MLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344


RESULT 2
NTRI_MOUSE
ID   NTRI_MOUSE     STANDARD;      PRT;   344 AA.
AC   Q99PJ0;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Neurotrimin precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ICR; TISSUE=Brain;
RA   Kim T.H., Choi S.C., Kim J., Jeon J.W., Kim K.D., Lee S.H.;
RT   "Cloning and expression of mouse neurotrimin gene in the developing
RT   nervous system.";
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Eye;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2).
CC   -!- FUNCTION: Neural cell adhesion molecule.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anch
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
CC       SUBFAMILY.
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaborati
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF282980; AAK00276.1; -.
DR   EMBL; BC023307; AAH23307.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00408; IGc2; 3.
DR   PROSITE; PS50835; IG_LIKE; 3.
KW   Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
KW   Repeat; Signal.
FT   SIGNAL        1     31       POTENTIAL.
FT   CHAIN        32    321       NEUROTRIMIN.
FT   PROPEP      322    344       REMOVED IN MATURE FORM (POTENTIAL).
FT   DOMAIN       39    126       IG-LIKE C2-TYPE 1.
FT   DOMAIN      136    218       IG-LIKE C2-TYPE 2.
FT   DOMAIN      222    309       IG-LIKE C2-TYPE 3.
FT   DISULFID     57    115       POTENTIAL.
FT   DISULFID    157    201       POTENTIAL.
FT   DISULFID    243    295       POTENTIAL.
FT   CARBOHYD     44     44       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     70     70       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    152    152       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    284    284       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    292    292       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    305    305       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    321    321       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   LIPID       321    321       GPI-ANCHOR (POTENTIAL).
FT   CONFLICT     75     75       L -> P (IN REF. 1).
FT   CONFLICT     92     92       S -> G (IN REF. 1).
FT   CONFLICT    119    119       T -> I (IN REF. 1).
FT   CONFLICT    187    187       E -> Q (IN REF. 1).
FT   CONFLICT    213    213       R -> P (IN REF. 1).
FT   CONFLICT    225    225       I -> F (IN REF. 1).
SQ   SEQUENCE   344 AA;  37984 MW;  C885BBA52C148554 CRC64;

  Query Match           91.2%;  Score 1647.5;  DB 1;  Length 344;
  Best Local Similarity   93.5%;  Pred. No. 3.8e-123;
  Matches  314;  Conservative    8;  Mismatches   11;  Indels    3;  Gaps    1;

Qy         12 ISWAIFTGLAALCLF---QGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAW 68
              : |    ::   ||    ||||||||||||||||||||||||||||||||||||||||
Db          9 LPWKCLVVVSLRLLFLVPTGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAW 68

Qy         69 LNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRV 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 LNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRV 128

Qy        129 HLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEI 188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 HLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEI 188

Qy        189 QGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAV 248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 11, 2003, 02:51:48 ; Search time 34 Seconds
(without alignments)
475.800 Million cell updates/sec

Title: US-10-017-084A-523
Perfect score: 1806
Sequence: 1 MKTIQPKMHNSISWAIFTGL.....RRAGCVWLLPLLVLHLLLKF 344

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1665.5	92.2	344	1	NTRI_HUMAN	Q9p121 homo sapien
2	1647.5	91.2	344	1	NTRI_MOUSE	Q99pj0 mus musculu
3	1639.5	90.8	344	1	NTRI_RAT	Q62718 rattus norv
4	1477.5	81.8	353	1	CEPU_CHICK	Q90773 gallus gall
5	1305	72.3	337	1	G55A_CHICK	Q98892 gallus gall
6	1268	70.2	345	1	OPCM_HUMAN	Q14982 homo sapien
7	1266	70.1	345	1	OPCM_BOVIN	P11834 bos taurus
8	1259	69.7	345	1	OPCM_RAT	P32736 rattus norv
9	938.5	52.0	338	1	LAMP_CHICK	Q98919 gallus gall
10	931.5	51.6	338	1	LAMP_HUMAN	Q13449 homo sapien
11	926.5	51.3	338	1	LAMP_RAT	Q62813 rattus norv
12	815	45.1	348	1	KILO_RAT	Q9z0j8 rattus norv
13	297.5	16.5	333	1	AMAL_DROME	P15364 drosophila
14	283.5	15.7	725	1	NCA2_MOUSE	P13594 mus musculu
15	283.5	15.7	1115	1	NCA1_MOUSE	P13595 mus musculu
16	279.5	15.5	1091	1	NCA1_CHICK	P13590 gallus gall
17	277.5	15.4	858	1	NCA1_RAT	P13596 rattus norv
18	277.5	15.4	1088	1	NCA1_XENLA	P16170 xenopus lae
19	276	15.3	761	1	NCA2_HUMAN	P13592 homo sapien
20	276	15.3	848	1	NCA1_HUMAN	P13591 homo sapien
21	275.5	15.3	853	1	NCA1_BOVIN	P31836 bos taurus
22	270.5	15.0	1092	1	NCA2_XENLA	P36335 xenopus lae
23	261.5	14.5	1010	1	CONT_CHICK	P14781 gallus gall
24	255	14.1	359	1	LACH_DROME	Q24372 drosophila
25	251.5	13.9	837	1	NCM2_MOUSE	O35136 mus musculu
26	250	13.8	349	1	LACH_SCHAM	Q26474 schistocerc
27	249.5	13.8	1040	1	AXO1_HUMAN	Q02246 homo sapien
28	246.5	13.6	1018	1	CONT_HUMAN	Q12860 homo sapien
29	243.5	13.5	1021	1	CONT_RAT	Q63198 rattus norv
30	243.5	13.5	1036	1	AXO1_CHICK	P28685 gallus gall
31	241.5	13.4	837	1	NCM2_HUMAN	O15394 homo sapien
32	241.5	13.4	1020	1	CONT_MOUSE	P12960 mus musculu
33	240	13.3	3707	1	PGBM_MOUSE	Q05793 mus musculu
34	234.5	13.0	1040	1	AXO1_RAT	P22063 rattus norv
35	229	12.7	4391	1	PGBM_HUMAN	P98160 homo sapien
36	227.5	12.6	1051	1	PTK7_CHICK	Q91048 gallus gall
37	226	12.5	6632	1	UN89_CAEEL	O01761 caenorhabdi
38	221.5	12.3	862	1	CD22_MOUSE	P35329 mus musculu
39	221	12.2	2012	1	DSCA_HUMAN	O60469 homo sapien
40	220.5	12.2	898	1	FAS2_SCHAM	P22648 schistocerc
41	215.5	11.9	1302	1	NRG_DROME	P20241 drosophila
42	211.5	11.7	873	1	FAS2_DROME	P34082 drosophila
43	211.5	11.7	1070	1	PTK7_HUMAN	Q13308 homo sapien
44	211.5	11.7	1461	1	NEO1_HUMAN	Q92859 homo sapien
45	210	11.6	1914	1	KMLS_HUMAN	Q15746 homo sapien

ALIGNMENTS

RESULT 1
NTRI_HUMAN
ID NTRI_HUMAN STANDARD; PRT; 344 AA.
AC Q9P121;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Neurotrimin precursor (hNT).
GN NT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Li G., Jin J., Tan X., Hu S., Yuan J., Qiang B.;
RT "Cloning and identification of human neurotrimin full length cDNA.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: Neural cell adhesion molecule.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
CC SUBFAMILY.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC ---

CC ---
DR EMBL; AF126426; AAF37591.1; -.
DR GO; GO:0008038; P:neuronal cell recognition; TAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00408; IGc2; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Immunoglobulin domain; Cell adhesion; G
KW Repeat; Signal.
FT SIGNAL 1 31 POTENTIAL.
FT CHAIN 32 321 NEUROTRIMI
FT PROPEP 322 344 REMOVED IN
FT DOMAIN 39 126 IG-LIKE C2
FT DOMAIN 136 218 IG-LIKE C2
FT DOMAIN 222 309 IG-LIKE C2
FT DISULFID 57 115 POTENTIAL.
FT DISULFID 157 201 POTENTIAL.
FT DISULFID 243 295 POTENTIAL.
FT CARBOHYD 44 44 N-LINKED (
FT CARBOHYD 70 70 N-LINKED (
FT CARBOHYD 152 152 N-LINKED (
FT CARBOHYD 284 284 N-LINKED (
FT CARBOHYD 292 292 N-LINKED (

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Db        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344


RESULT 15
AAM40499
ID   AAM40499 standard; Protein; 355 AA.
XX
AC   AAM40499;
XX
DT   22-OCT-2001  (first entry)
XX
DE   Human polypeptide SEQ ID NO 5430.
XX
KW   Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW   peripheral nervous system; neuropathy; central nervous system; CNS;
KW   Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW   amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW   chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW   leukaemia.
XX
OS   Homo sapiens.
XX
PN   WO200153312-A1.
XX
PD   26-JUL-2001.
XX
PF   26-DEC-2000; 2000WO-US34263.
XX
PR   21-JAN-2000; 2000US-0488725.
PR   25-APR-2000; 2000US-0552317.
PR   09-JUL-2000; 2000US-0598042.
PR   19-JUL-2000; 2000US-0620312.
PR   03-AUG-2000; 2000US-0653450.
PR   14-SEP-2000; 2000US-0662191.
PR   19-OCT-2000; 2000US-0693036.
PR   29-NOV-2000; 2000US-0727344.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Asundi V,  Chen R,  Ma Y,  Qian XB,  Ren F,  Wang D;
PI   Wang J,  Wang Z,  Wehrman T,  Xu C,  Xue AJ,  Yang Y,  Zhang J;
PI   Zhao QA,  Zhou P,  Goodrich R,  Drmanac RT;
XX
DR   WPI; 2001-442253/47.
DR   N-PSDB; AAI59655.
XX
PT   Novel nucleic acids and polypeptides, useful for treating disorders
PT   such as central nervous system injuries -
XX
PS   Example 2; SEQ ID NO 5430; 10078pp; English.
XX
CC   The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC   the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC   immunosuppressant and cytostatic activity. The polynucleotides are useful
CC   in gene therapy. A composition containing a polypeptide or polynucleotide
CC   of the invention may be used to treat diseases of the peripheral nervous
CC   system, such as peripheral nervous injuries, peripheral neuropathy and
CC   localised neuropathies and central nervous system diseases, such as
CC   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC   lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC   utilisation of the activities such as: Immune system suppression,
CC   Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC   assays for receptor activity, arthritis and inflammation, leukaemias and
CC   C.N.S disorders.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification.
XX
SQ   Sequence   355 AA;

  Query Match           100.0%;  Score 1806;  DB 22;  Length 355;
  Best Local Similarity  100.0%;  Pred. No. 3.2e-149;
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  Matches  344;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60
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Db         12 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 71

Qy         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 131

Qy        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 191

Qy        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 251

Qy        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 311

Qy        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
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Db        312 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 355


Search completed: September 11, 2003, 03:02:43
Job time : 74 secs
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PR 16-DEC-1999; 99WO-US30095.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 24-FEB-2000; 2000WO-US05004.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 24-AUG-2000; 2000WO-US23328.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 22-MAR-2001; 2001WO-US09552.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 17-OCT-1997; 97US-062250P.
PR 03-NOV-1997; 97US-064249P.
PR 13-NOV-1997; 97US-065311P.
PR 21-NOV-1997; 97US-066364P.
PR 10-MAR-1998; 98US-077450P.
PR 11-MAR-1998; 98US-077632P.
PR 11-MAR-1998; 98US-077641P.
PR 11-MAR-1998; 98US-077649P.
PR 12-MAR-1998; 98US-077791P.
PR 13-MAR-1998; 98US-078004P.
PR 20-MAR-1998; 98US-078886P.
PR 20-MAR-1998; 98US-078910P.
PR 20-MAR-1998; 98US-078936P.
PR 20-MAR-1998; 98US-078939P.
PR 25-MAR-1998; 98US-079294P.
PR 26-MAR-1998; 98US-079656P.
PR 27-MAR-1998; 98US-079663P.
PR 27-MAR-1998; 98US-079664P.
PR 27-MAR-1998; 98US-079689P.
PR 27-MAR-1998; 98US-079728P.
PR 27-MAR-1998; 98US-079786P.
PR 30-MAR-1998; 98US-079920P.
PR 30-MAR-1998; 98US-079923P.
PR 26-MAY-1981; 81US-0267213.
PR 17-MAR-1998; 98US-0040220.
PR 26-JUN-1998; 98US-0105413.
PR 07-OCT-1998; 98US-0168978.
PR 02-NOV-1998; 98US-0184216.
PR 06-NOV-1998; 98US-0187368.
PR 07-DEC-1998; 98US-0202054.
PR 22-DEC-1998; 98US-0218517.
PR 05-MAR-1999; 99US-0254465.
PR 10-MAR-1999; 99US-0265686.
PR 12-APR-1999; 99US-0284291.
PR 14-MAY-1999; 99US-0311832.
PR 14-MAY-1999; 99US-0380137.
PR 25-AUG-1999; 99US-0380138.
PR 25-AUG-1999; 99US-0380142.
PR 08-NOV-2000; 2000US-0709238.
PR 27-NOV-2000; 2000US-0723749.
PR 20-DEC-2000; 2000US-0747259.
PR 22-MAR-2001; 2001US-0816744.
PR 22-MAR-2001; 2001US-0816920.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 30-JUL-2001; 2001US-0918585.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi A, Baker KP, Botstein D, Desnoyers L, Eaton D;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2003-288163/28.
DR N-PSDB; ABX92696.
XX
PT Novel secreted and transmembrane polypeptides and polynucleotides
PT encoding them useful for treating cancer, kidney diseases, bone,
PT cartilage disorders and immune deficiencies
XX
PS Claim 12; Fig 222; 459pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The
CC PRO polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for
CC linking bioactive molecules to cells expressing PRO polypeptides,
CC for modulating biological activities of cells expressing PRO
CC polypeptides, and for for identifying agonists or antagonists. The
CC bioactive molecule maybe a toxin, radiolabel or antibody, and causes
CC apoptosis or death of the cell. The PRO polypeptides are useful for
CC treating immune disorders, diabetes or hyper- or hypo-insulinaemia,
CC cardiac insufficiency, nervous system disorders, kidney disorders,
CC bone and cartilage disorders or arthritis, tumours, and wound healing.
CC The polynucleotide sequences encoding PRO polypeptides are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, in the preparation of PRO polypeptides, for
CC generating transgenic animals or knockout animals, for the genetic
CC analysis of individuals with genetic disorders, and in gene therapy.
CC ABU61071-ABU61164 represent the human PRO polypeptides of the
CC invention.
CC Note: The sequence data for this patent was obtained in electronic
CC format directly from the USPTO web site at
CC seqdata.uspto.gov/psipsDIDEntry.html.
XX
SQ Sequence 344 AA;

Query Match 100.0%; Score 1806; DB 24; Length 344;
Best Local Similarity 100.0%; Pred. No. 3e-149;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60

Qy         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120

Qy        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180

Qy        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240

Qy        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300

Qy        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
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PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 20-DEC-2000; 2000US-0747259.
PR 28-FEB-2001; 2001US-0796498.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 18-MAY-2001; 2001US-0860216.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 21-JUN-2001; 2001US-0887879.
PR 18-JUL-2001; 2001US-0908827.
PR 06-AUG-2001; 2001US-0924419.
PR 09-AUG-2001; 2001US-0927796.
PR 16-AUG-2001; 2001US-0931836.
PR 19-DEC-2001; 2001US-0028072.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-148238/14.
DR N-PSDB; ABX89328.
XX
PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT are therapeutically useful for enhancing immune response and in cancer
PT treatments
XX
PS Claim 12; Fig 376; 659pp; English.
XX
CC The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813
CC and PRO11066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpetiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and
CC are thus useful for treating sports injuries, and arthritis. This
CC is the amino acid sequence of a novel human PRO protein.
XX
SQ Sequence 344 AA;

Query Match 100.0%; Score 1806; DB 24; Length 344;
Best Local Similarity 100.0%; Pred. No. 3e-149;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60
Db 1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60

Qy 61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120
Db 61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120

Qy 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180
Db 121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180

Qy 181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240
Db 181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240

Qy 241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300
Db 241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300

Qy 301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
Db 301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344

RESULT 14
ABU61159
ID ABU61159 standard; Protein; 344 AA.
XX
AC ABU61159;
XX
DT 08-MAY-2003 (first entry)
XX
DE Human PRO337 polypeptide.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;
KW cardiac insufficiency; nervous system disorder; kidney disorder;
KW bone disorder; cartilage disorder; arthritis; tumour; wound healing;
KW genetic disorder; cytostatic; antidiabetic; antiinflammatory;
KW antiarthritic; anti-tumour; vulnerary; antianaemic; dermatological;
KW cardiant.
XX
OS Homo sapiens.
XX
PN US2002169284-A1.
XX
PD 14-NOV-2002.
XX
PF 16-OCT-2001; 2001US-0978697.
XX
PR 07-OCT-1998; 98WO-US21141.
PR 20-NOV-1998; 98WO-US24855.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US05190.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 30-NOV-1999; 99WO-US28313.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28565.

CC linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a
CC cell expressing the polypeptides. The bioactive molecule causes cell
CC death. (II) Is useful as hybridisation probes, in chromosome and gene
CC mapping, in generation of antisense RNA and DNA, in the preparation of
CC PRO polypeptide, for generating transgenic animals or knockout animals
CC which in turn are useful in the development and screening of
CC therapeutically useful reagents, and for the genetic analysis of
CC individuals with genetic disorders, in gene therapy, and for chromosome
CC identification. (I) Or Ab is useful for the preparation of medicament for
CC treating conditions which are responsive to the PRO polypeptide or
CC anti-PRO antibody e.g. a tumour. (I) is useful for treating obesity,
CC diabetes or hypo- or hyper-insulinaemia, and cardiac insufficiency
CC disorders, for inhibiting tumour growth, enhances vascular permeability
CC and immune response, for inducing regeneration of auditory hair cells and
CC for treating hearing loss in mammals, and for treating bone and/or
CC cartilage disorders such as sports injuries and arthritis. This is the
CC amino acid sequence of a novel human secreted and transmembrane
CC polypeptide associated oligonucleotide.
XX
SQ Sequence 344 AA;

Query Match 100.0%; Score 1806; DB 24; Length 344;
Best Local Similarity 100.0%; Pred. No. 3e-149;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60

Qy         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120

Qy        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180

Qy        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240

Qy        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300

Qy        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
              |||||||||||||||||||||||||||||||||||||||||||
Db        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
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RESULT 13
ABU59838
ID ABU59838 standard; Protein; 344 AA.
XX
AC ABU59838;
XX
DT 13-MAY-2003 (first entry)
XX
DE Novel secreted and transmembrane protein PRO337.
XX
KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosum; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpetiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis.
XX
OS Homo sapiens.
XX
PN US2003017563-A1.
XX
PD 23-JAN-2003.
XX
PF 07-MAY-2002; 2002US-0140808.
XX
PR 31-MAR-1997; 97WO-US05230.
PR 12-JUN-1998; 98WO-US12456.
PR 14-JUL-1998; 98WO-US14552.
PR 28-AUG-1998; 98WO-US17888.
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19093.
PR 14-SEP-1998; 98WO-US19094.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 29-OCT-1998; 98WO-US22991.
PR 29-OCT-1998; 98WO-US22992.
PR 20-NOV-1998; 98WO-US24855.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US05190.
PR 20-APR-1999; 99WO-US08615.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 22-DEC-1999; 99WO-US30720.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05746.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.

```
Qy        61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120

Qy       121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180

Qy       181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240

Qy       241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300

Qy       301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
             |||||||||||||||||||||||||||||||||||||||||||||
Db       301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
```

RESULT 12
ABU67293
ID ABU67293 standard; Protein; 344 AA.
XX
AC ABU67293;
XX
DT 28-MAY-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO337.
XX
KW Secreted and transmembrane polypeptide; PRO polypeptide; PRO533;
KW PRO301; PRO187; PRO337; PRO1411; PRO10096; PRO246; PRO6307; PRO6003;
KW PRO6004; PRO4356; PRO2630; PRO265; PRO941; FGFR; bioactive molecule;
KW fibroblast growth factor receptor; cell death; chromosome mapping;
KW gene mapping; transgenic animal; knockout animal; gene therapy;
KW tumour; obesity; diabetes; insulinaemia; vascular permeability;
KW cardiac insufficiency disorder; immune response; hearing loss;
KW auditory hair cell regeneration; bone disorder; cartilage disorder;
KW sports injury; arthritis.
XX
OS Homo sapiens.
XX
PN US2003032063-A1.
XX
PD 13-FEB-2003.
XX
PF 01-FEB-2002; 2002US-0066494.
XX
PR 14-SEP-1998; 98WO-US19093.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 20-NOV-1998; 98WO-US24855.
PR 25-NOV-1998; 98WO-US25190.
PR 01-DEC-1998; 98WO-US25108.
PR 08-MAR-1999; 99WO-US05028.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28565.
PR 20-DEC-1999; 99WO-US30999.
PR 05-JAN-2000; 2000WO-US00219.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 09-MAR-2000; 2000WO-US06471.
PR 20-MAR-2000; 2000WO-US07377.
PR 30-MAR-2000; 2000WO-US08439.
PR 15-MAY-2000; 2000WO-US13358.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 01-DEC-2000; 2000WO-US32678.
PR 28-FEB-2001; 2001WO-US06520.
PR 30-MAY-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 26-AUG-1997; 97US-056974P.
PR 17-SEP-1997; 97US-059115P.
PR 18-SEP-1997; 97US-059263P.
PR 19-SEP-1997; 97US-059588P.
PR 17-OCT-1997; 97US-062285P.
PR 24-OCT-1997; 97US-062816P.
PR 24-OCT-1997; 97US-063082P.
PR 27-OCT-1997; 97US-063329P.
PR 29-OCT-1997; 97US-063733P.
PR 21-NOV-1997; 97US-066364P.
PR 25-NOV-1997; 97US-066840P.
PR 16-DEC-1997; 97US-069694P.
PR 09-FEB-1998; 98US-074086P.
PR 09-FEB-1998; 98US-074092P.
PR 25-MAR-1998; 98US-079294P.
PR 08-APR-1998; 98US-081049P.
PR 10-AUG-1998; 98US-095998P.
PR 18-AUG-1998; 98US-097000P.
PR 09-SEP-1998; 98US-099601P.
PR 10-SEP-1998; 98US-099803P.
PR 10-SEP-1998; 98US-099811P.
PR 10-SEP-1998; 98US-099812P.
PR 17-SEP-1998; 98US-100858P.
PR 24-SEP-1998; 98US-101922P.
PR 28-OCT-1998; 98US-106032P.
PR 20-NOV-1998; 98US-109304P.
PR 23-MAR-1999; 99US-125778P.
PR 15-JUN-1999; 99US-139695P.
PR 20-JUL-1999; 99US-145070P.
PR 26-JUL-1999; 99US-145698P.
PR 17-AUG-1999; 99US-149396P.
PR 07-DEC-1999; 99US-169495P.
PR 15-NOV-2001; 2001US-0002796.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;
XX
DR WPI; 2003-341964/32.
DR N-PSDB; ACA04996.
XX
PT Thirty seven nucleic acids encoding novel secreted and transmembrane
PT PRO polypeptides, useful for modulating biological activity of cell
PT expressing the polypeptide, and in chromosome and gene mapping -
XX
PS Claim 12; Fig 52; 255pp; English.
XX
CC The invention describes an isolated, secreted and transmembrane
CC polypeptide (I), termed PRO polypeptide. (I) Is useful for detecting
CC PRO533, PRO301, PRO187, PRO337, PRO1411, PRO10096, PRO246, PRO6307,
CC PRO6003, PRO6004, PRO4356, PRO2630, PRO265, PRO941, fibroblast growth
CC factor receptor (FGFR)-4, FGFR-3, FGFR-2 or FGFR-1 polypeptide, and for

```
DE   Novel human secreted and transmembrane protein PRO337.
XX
KW   Secreted and transmembrane polypeptide; PRO polypeptide; PRO533;
KW   PRO301; PRO187; PRO337; PRO1411; PRO10096; PRO246; PRO6307; PRO6003;
KW   PRO6004; PRO4356; PRO2630; PRO265; PRO941; FGFR; bioactive molecule;
KW   fibroblast growth factor receptor; cell death; chromosome mapping;
KW   gene mapping; transgenic animal; knockout animal; gene therapy;
KW   tumour; obesity; diabetes; insulinaemia; vascular permeability;
KW   cardiac insufficiency disorder; immune response; hearing loss;
KW   auditory hair cell regeneration; bone disorder; cartilage disorder;
KW   sports injury; arthritis.
XX
OS   Homo sapiens.
XX
PN   US2003032062-A1.
XX
PD   13-FEB-2003.
XX
PF   01-FEB-2002; 2002US-0066273.
XX
PR   14-JUL-1998;   98WO-US14552.
PR   10-SEP-1998;   98WO-US18824.
PR   14-SEP-1998;   98WO-US19093.
PR   16-SEP-1998;   98WO-US19330.
PR   17-SEP-1998;   98WO-US19437.
PR   20-NOV-1998;   98WO-US24855.
PR   25-NOV-1998;   98WO-US25190.
PR   01-DEC-1998;   98WO-US25108.
PR   08-MAR-1999;   99WO-US05028.
PR   02-JUN-1999;   99WO-US12252.
PR   01-SEP-1999;   99WO-US20111.
PR   08-SEP-1999;   99WO-US20594.
PR   15-SEP-1999;   99WO-US21090.
PR   15-SEP-1999;   99WO-US21547.
PR   30-NOV-1999;   99WO-US28313.
PR   01-DEC-1999;   99WO-US28301.
PR   02-DEC-1999;   99WO-US28565.
PR   20-DEC-1999;   99WO-US30999.
PR   05-JAN-2000; 2000WO-US00219.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   22-FEB-2000; 2000WO-US04414.
PR   01-MAR-2000; 2000WO-US05601.
PR   02-MAR-2000; 2000WO-US05841.
PR   09-MAR-2000; 2000WO-US06471.
PR   20-MAR-2000; 2000WO-US07377.
PR   30-MAR-2000; 2000WO-US08439.
PR   15-MAY-2000; 2000WO-US13358.
PR   17-MAY-2000; 2000WO-US13705.
PR   22-MAY-2000; 2000WO-US14042.
PR   30-MAY-2000; 2000WO-US14941.
PR   02-JUN-2000; 2000WO-US15264.
PR   11-AUG-2000; 2000WO-US22031.
PR   23-AUG-2000; 2000WO-US23522.
PR   24-AUG-2000; 2000WO-US23328.
PR   01-DEC-2000; 2000WO-US32678.
PR   28-FEB-2001; 2001WO-US06520.
PR   30-MAY-2001; 2001WO-US17443.
PR   01-JUN-2001; 2001WO-US17800.
PR   20-JUN-2001; 2001WO-US19692.
PR   29-JUN-2001; 2001WO-US21066.
PR   09-JUL-2001; 2001WO-US21735.
PR   26-AUG-1997;   97US-056974P.
PR   17-SEP-1997;   97US-059115P.
PR   18-SEP-1997;   97US-059263P.
PR   19-SEP-1997;   97US-059588P.
PR   17-OCT-1997;   97US-062285P.
PR   24-OCT-1997;   97US-062816P.
PR   24-OCT-1997;   97US-063082P.
PR   27-OCT-1997;   97US-063329P.
PR   29-OCT-1997;   97US-063733P.
PR   21-NOV-1997;   97US-066364P.
PR   25-NOV-1997;   97US-066840P.
PR   16-DEC-1997;   97US-069694P.
PR   09-FEB-1998;   98US-074086P.
PR   09-FEB-1998;   98US-074092P.
PR   25-MAR-1998;   98US-079294P.
PR   08-APR-1998;   98US-081049P.
PR   10-AUG-1998;   98US-095998P.
PR   18-AUG-1998;   98US-097000P.
PR   09-SEP-1998;   98US-099601P.
PR   10-SEP-1998;   98US-099803P.
PR   10-SEP-1998;   98US-099811P.
PR   10-SEP-1998;   98US-099812P.
PR   17-SEP-1998;   98US-100858P.
PR   24-SEP-1998;   98US-101922P.
PR   28-OCT-1998;   98US-106032P.
PR   20-NOV-1998;   98US-109304P.
PR   23-MAR-1999;   99US-125778P.
PR   15-JUN-1999;   99US-139695P.
PR   20-JUL-1999;   99US-145070P.
PR   26-JUL-1999;   99US-145698P.
PR   17-AUG-1999;   99US-149396P.
PR   07-DEC-1999;   99US-169495P.
PR   15-NOV-2001; 2001US-0002796.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Botstein DA,  Desnoyers L,  Eaton DL;
PI   Ferrara N,  Fong S,  Gao W,  Gerber H,  Gerritsen ME,  Goddard A;
PI   Godowski PJ,  Gurney AL,  Kljavin IJ,  Mather JP,  Napier MA,  Pan J;
PI   Paoni NF,  Roy MA,  Stewart TA,  Tumas D,  Watanabe CK,  Williams PM;
PI   Wood WI,  Zhang Z;
XX
DR   WPI; 2003-341963/32.
DR   N-PSDB; ACA04516.
XX
PT   New secreted and transmembrane polypeptide for modulating biological
PT   activity of a cell expressing the polypeptide, identifying agonists or
PT   antagonists of the polypeptide, and as molecular weight markers
XX
PS   Claim 12; Fig 52; 254pp; English.
XX
CC   The invention describes an isolated, secreted and transmembrane
CC   polypeptide (I), termed PRO polypeptide. (I) Is useful for detecting
CC   PRO533, PRO301, PRO187, PRO337, PRO1411, PRO10096, PRO246, PRO6307,
CC   PRO6003, PRO6004, PRO4356, PRO2630, PRO265, PRO941, fibroblast growth
CC   factor receptor (FGFR)-4, FGFR-3, FGFR-2 or FGFR-1 polypeptide, and for
CC   linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a
CC   cell expressing the polypeptides. The bioactive molecule causes cell
CC   death. (II) Is useful as hybridisation probes, in chromosome and gene
CC   mapping, in generation of antisense RNA and DNA, in the preparation of
CC   PRO polypeptide, for generating transgenic animals or knockout animals
CC   which in turn are useful in the development and screening of
CC   therapeutically useful reagents, and for the genetic analysis of
CC   individuals with genetic disorders, in gene therapy, and for chromosome
CC   identification. (I) Or Ab is useful for the preparation of medicament for
CC   treating conditions which are responsive to the PRO polypeptide or
CC   anti-PRO antibody e.g. a tumour. (I) is useful for treating obesity,
CC   diabetes or hypo- or hyper-insulinaemia, and cardiac insufficiency
CC   disorders, for inhibiting tumour growth, enhances vascular permeability
CC   and immune response, for inducing regeneration of auditory hair cells and
CC   for treating hearing loss in mammals, and for treating bone and/or
CC   cartilage disorders such as sports injuries and arthritis. This is the
CC   amino acid sequence of a novel human secreted and transmembrane
CC   polypeptide.
XX
SQ   Sequence   344 AA;

  Query Match          100.0%;  Score 1806;  DB 24;  Length 344;
  Best Local Similarity  100.0%;  Pred. No. 3e-149;
  Matches  344;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60
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PR   30-DEC-1999;   99WO-US31274.
PR   05-JAN-2000; 2000WO-US00219.
PR   06-JAN-2000; 2000WO-US00277.
PR   06-JAN-2000; 2000WO-US00376.
PR   11-FEB-2000; 2000WO-US03565.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   22-FEB-2000; 2000WO-US04414.
PR   24-FEB-2000; 2000WO-US04914.
PR   24-FEB-2000; 2000WO-US05004.
PR   01-MAR-2000; 2000WO-US05601.
PR   02-MAR-2000; 2000WO-US05746.
PR   02-MAR-2000; 2000WO-US05841.
PR   10-MAR-2000; 2000WO-US06319.
PR   15-MAR-2000; 2000WO-US06884.
PR   20-MAR-2000; 2000WO-US07377.
PR   21-MAR-2000; 2000WO-US07532.
PR   30-MAR-2000; 2000WO-US08439.
PR   17-MAY-2000; 2000WO-US13705.
PR   22-MAY-2000; 2000WO-US14042.
PR   30-MAY-2000; 2000WO-US14941.
PR   02-JUN-2000; 2000WO-US15264.
PR   28-JUL-2000; 2000WO-US20710.
PR   11-AUG-2000; 2000WO-US22031.
PR   23-AUG-2000; 2000WO-US23522.
PR   24-AUG-2000; 2000WO-US23328.
PR   08-NOV-2000; 2000WO-US30952.
PR   10-NOV-2000; 2000WO-US30873.
PR   01-DEC-2000; 2000WO-US32678.
PR   20-DEC-2000; 2000WO-US34956.
PR   28-FEB-2001; 2001WO-US06520.
PR   01-MAR-2001; 2001WO-US06666.
PR   25-MAY-2001; 2001WO-US17092.
PR   01-JUN-2001; 2001WO-US17800.
PR   20-JUN-2001; 2001WO-US19692.
PR   22-JUN-2001; 2001WO-US20116.
PR   29-JUN-2001; 2001WO-US21066.
PR   09-JUL-2001; 2001WO-US21735.
PR   20-DEC-2000; 2000US-0747259.
PR   28-FEB-2001; 2001US-0796498.
PR   09-MAR-2001; 2001US-0802706.
PR   14-MAR-2001; 2001US-0808689.
PR   22-MAR-2001; 2001US-0816744.
PR   05-APR-2001; 2001US-0828366.
PR   10-MAY-2001; 2001US-0854208.
PR   10-MAY-2001; 2001US-0854280.
PR   18-MAY-2001; 2001US-0860216.
PR   25-MAY-2001; 2001US-0866028.
PR   25-MAY-2001; 2001US-0866034.
PR   01-JUN-2001; 2001US-0872035.
PR   05-JUN-2001; 2001US-0874503.
PR   14-JUN-2001; 2001US-0882636.
PR   19-JUN-2001; 2001US-0886342.
PR   21-JUN-2001; 2001US-0887879.
PR   18-JUL-2001; 2001US-0908827.
PR   06-AUG-2001; 2001US-0924419.
PR   09-AUG-2001; 2001US-0927796.
PR   16-AUG-2001; 2001US-0931836.
PR   19-DEC-2001; 2001US-0028072.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Beresini M,  DeForge L,  Desnoyers L,  Filvaroff E,  Gao W;
PI   Gerritsen ME,  Goddard A,  Godowski PJ,  Gurney AL,  Sherwood S;
PI   Smith V,  Stewart TA,  Tumas D,  Watanabe CK,  Wood WI,  Zhang Z;
XX
DR   WPI; 2003-331925/31.
DR   N-PSDB; ACA04211.
XX
PT   New secreted and transmembrane nucleic acids and polypeptides,
PT   designated as PRO, useful for treating inflammation, organ failure,
PT   atherosclerosis, cardiac injury, infertility, birth defects, premature
PT   aging, AIDS, or cancer -
XX
PS   Claim 12; Fig 376; 659pp; English.
XX
CC   The invention relates to an isolated nucleic acid comprising, or which is
CC   at least 80% identical to, or the full-length coding sequence of, any of
CC   the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
CC   (one of 275 secreted or transmembrane proteins). The nucleic acid
CC   further comprises the full-length coding sequence of the DNA deposited
CC   under American Type Culture Collection (ATCC) accession number in a list
CC   given in the specification. Also included are vectors and host
CC   cells for producing PRO proteins, PRO fusion proteins, anti-PRO
CC   antibodies, PRO extracellular domains and mature sequences, methods
CC   of detecting PRO proteins, methods for stimulating the release of
CC   TNF-alpha (tumour necrosis factor alpha) from human blood,
CC   (and the proliferation of differentiation of chondrocyte cells, the
CC   proliferation of, or gene expression in pericyte cells, the release or
CC   proteoglycans from cartilage, proliferation of inner ear urticular
CC   supporting cells, the proliferation of T-lymphocyte cells, the release
CC   of a cytokine from peripheral blood mononuclear cells (PBMC), or the
CC   proliferation of endothelial cells), a method for modulating the uptake
CC   of glucose or free fatty acid (FFA) by skeletal muscle cells,
CC   a method for inhibiting the binding of A-peptide to factor VIIA,
CC   or the differentiation of adipocyte cells, a method for detecting the
CC   presence of a tumour in a mammal and an oligonucleotide probe derived
CC   from any of the nucleotide sequences cited above. The nucleic acids and
CC   polypeptides are useful for treating inflammatory diseases, organ
CC   failure, atherosclerosis, cardiac injury, infertility, birth defects,
CC   premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or
CC   diabetic complications. The nucleic acids are useful as hybridisation
CC   probes, in chromosome and gene mapping, and in generating antisense RNA
CC   or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
CC   biosensors or bioreactors. Both are useful in tissue typing.
CC   The present sequence represents a PRO protein of the invention.
XX
SQ   Sequence   344 AA;

  Query Match           100.0%;  Score 1806;  DB 24;  Length 344;
  Best Local Similarity  100.0%;  Pred. No. 3e-149;
  Matches  344;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60

Qy         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120

Qy        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180

Qy        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240

Qy        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300

Qy        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
              |||||||||||||||||||||||||||||||||||||||||||||
Db        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344


RESULT 11
ABU67162
ID   ABU67162 standard; Protein; 344 AA.
XX
AC   ABU67162;
XX
DT   28-MAY-2003  (first entry)
XX
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PR   10-MAY-2001; 2001US-0854280.
PR   18-MAY-2001; 2001US-0860216.
PR   25-MAY-2001; 2001US-0866028.
PR   25-MAY-2001; 2001US-0866034.
PR   01-JUN-2001; 2001US-0872035.
PR   05-JUN-2001; 2001US-0874503.
PR   14-JUN-2001; 2001US-0882636.
PR   19-JUN-2001; 2001US-0886342.
PR   21-JUN-2001; 2001US-0887879.
PR   18-JUL-2001; 2001US-0908827.
PR   06-AUG-2001; 2001US-0924419.
PR   09-AUG-2001; 2001US-0927796.
PR   16-AUG-2001; 2001US-0931836.
PR   19-DEC-2001; 2001US-0028072.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
PI   Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI   Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR   WPI; 2003-332040/31.
DR   N-PSDB; ACA03790.
XX
PT   New secreted and transmembrane PRO nucleic acids, useful for gene
PT   therapy, in chromosome and gene mapping, as chromosome markers, in
PT   tissue typing, and in chromosome identification -
XX
PS   Claim 12; Fig 376; 660pp; English.
XX
CC   The present invention relates to the isolation of novel human PRO
CC   polypeptides, and the polynucleotide sequences encoding them. The
CC   PRO polypeptides are secreted and transmembrane proteins. The PRO
CC   polypeptides are useful for detecting other PRO polypeptides, for
CC   linking bioactive molecules to cells expressing PRO polypeptides,
CC   for modulating biological activities of cells expressing PRO
CC   polypeptides, and for for identifying agonists or antagonists.
CC   The PRO polypeptides are useful for for stimulating the release of
CC   tumour necrosis factor (TNF)-alpha from human blood, for stimulating
CC   the proliferation or differentiation of chondrocytes, and detecting the
CC   presence of tumours. The polynucleotide sequences encoding PRO
CC   polypeptides are useful as hybridisation probes, in chromosome and
CC   gene mapping, in the generation of antisense RNA and DNA, in the
CC   preparation of PRO polypeptides, for generating transgenic animals or
CC   knockout animals, for the genetic analysis of individuals with genetic
CC   disorders, and in gene therapy. ABU66570-ABU66844 represent the human
CC   PRO polypeptides of the invention.
CC   Note: The sequence data for this patent was obtained in electronic
CC   format directly from the USPTO web site at
CC   seqdata.uspto.gov/psipsDIDEntry.html.
XX
SQ   Sequence  344 AA;

  Query Match           100.0%;  Score 1806;  DB 24;  Length 344;
  Best Local Similarity  100.0%;  Pred. No. 3e-149;
  Matches  344;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60

Qy         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120

Qy        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180

Qy        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240

Qy        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300

Qy        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
              |||||||||||||||||||||||||||||||||||||||||||||
Db        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344


RESULT 10
ABU67033
ID   ABU67033 standard; Protein; 344 AA.
XX
AC   ABU67033;
XX
DT   27-MAY-2003  (first entry)
XX
DE   Human secreted/transmembrane, PRO, protein SEQ ID 376.
XX
KW   Human; secreted protein; transmembrane protein; PRO;
KW   inflammatory disease; organ failure; atherosclerosis; cardiac injury;
KW   infertility; birth defects; premature aging; AIDS; biosensor;
KW   acquired immunodeficiency syndrome; cancer; diabetic complication;
KW   bioreactor; tumour.
XX
OS   Homo sapiens.
XX
PN   US2003032155-A1.
XX
PD   13-FEB-2003.
XX
PF   03-MAY-2002; 2002US-0137865.
XX
PR   31-MAR-1997;   97WO-US05230.
PR   12-JUN-1998;   98WO-US12456.
PR   14-JUL-1998;   98WO-US14552.
PR   28-AUG-1998;   98WO-US17888.
PR   10-SEP-1998;   98WO-US18824.
PR   14-SEP-1998;   98WO-US19093.
PR   14-SEP-1998;   98WO-US19094.
PR   14-SEP-1998;   98WO-US19177.
PR   16-SEP-1998;   98WO-US19330.
PR   17-SEP-1998;   98WO-US19437.
PR   07-OCT-1998;   98WO-US21141.
PR   29-OCT-1998;   98WO-US22991.
PR   29-OCT-1998;   98WO-US22992.
PR   20-NOV-1998;   98WO-US24855.
PR   01-DEC-1998;   98WO-US25108.
PR   05-JAN-1999;   99WO-US00106.
PR   08-MAR-1999;   99WO-US05028.
PR   10-MAR-1999;   99WO-US05190.
PR   20-APR-1999;   99WO-US08615.
PR   14-MAY-1999;   99WO-US10733.
PR   02-JUN-1999;   99WO-US12252.
PR   01-SEP-1999;   99WO-US20111.
PR   08-SEP-1999;   99WO-US20594.
PR   13-SEP-1999;   99WO-US20944.
PR   15-SEP-1999;   99WO-US21090.
PR   15-SEP-1999;   99WO-US21547.
PR   05-OCT-1999;   99WO-US23089.
PR   29-NOV-1999;   99WO-US28214.
PR   30-NOV-1999;   99WO-US28313.
PR   30-NOV-1999;   99WO-US28409.
PR   01-DEC-1999;   99WO-US28301.
PR   01-DEC-1999;   99WO-US28634.
PR   02-DEC-1999;   99WO-US28551.
PR   02-DEC-1999;   99WO-US28564.
PR   02-DEC-1999;   99WO-US28565.
PR   16-DEC-1999;   99WO-US30095.
PR   20-DEC-1999;   99WO-US30911.
PR   20-DEC-1999;   99WO-US30999.
PR   22-DEC-1999;   99WO-US30720.
PR   30-DEC-1999;   99WO-US31243.
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```
CC   construct hybridisation probes for mapping the gene which encodes the
CC   PRO and for the genetic analysis of individuals with genetic disorders,
CC   in gene therapy, for chromosome identification and as a chromosome
CC   marker. (I) and (II) are useful for tissue typing. This is the amino
CC   acid sequence of a novel human secreted and transmembrane PRO
CC   polypeptide.
XX
SQ   Sequence   344 AA;

  Query Match           100.0%;  Score 1806;  DB 24;  Length 344;
  Best Local Similarity  100.0%;  Pred. No. 3e-149;
  Matches  344;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60

Qy         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120

Qy        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180

Qy        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240

Qy        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300

Qy        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
              |||||||||||||||||||||||||||||||||||||||||||
Db        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344


RESULT 9
ABU66757
ID   ABU66757 standard; Protein; 344 AA.
XX
AC   ABU66757;
XX
DT   23-MAY-2003  (first entry)
XX
DE   Human PRO polypeptide #188.
XX
KW   Human; PRO polypeptide; secreted and transmembrane protein;
KW   tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
KW   differentiation; chondrocyte; tumour; genetic disorder;
KW   cytostatic.
XX
OS   Homo sapiens.
XX
PN   US2003036180-A1.
XX
PD   20-FEB-2003.
XX
PF   09-MAY-2002; 2002US-0143114.
XX
PR   31-MAR-1997;   97WO-US05230.
PR   12-JUN-1998;   98WO-US12456.
PR   14-JUL-1998;   98WO-US14552.
PR   28-AUG-1998;   98WO-US17888.
PR   10-SEP-1998;   98WO-US18824.
PR   14-SEP-1998;   98WO-US19093.
PR   14-SEP-1998;   98WO-US19094.
PR   14-SEP-1998;   98WO-US19177.
PR   16-SEP-1998;   98WO-US19330.
PR   17-SEP-1998;   98WO-US19437.
PR   07-OCT-1998;   98WO-US21141.
PR   29-OCT-1998;   98WO-US22991.
PR   29-OCT-1998;   98WO-US22992.
PR   20-NOV-1998;   98WO-US24855.
PR   01-DEC-1998;   98WO-US25108.
PR   05-JAN-1999;   99WO-US00106.
PR   08-MAR-1999;   99WO-US05028.
PR   10-MAR-1999;   99WO-US05190.
PR   20-APR-1999;   99WO-US08615.
PR   14-MAY-1999;   99WO-US10733.
PR   02-JUN-1999;   99WO-US12252.
PR   01-SEP-1999;   99WO-US20111.
PR   08-SEP-1999;   99WO-US20594.
PR   13-SEP-1999;   99WO-US20944.
PR   15-SEP-1999;   99WO-US21090.
PR   15-SEP-1999;   99WO-US21547.
PR   05-OCT-1999;   99WO-US23089.
PR   29-NOV-1999;   99WO-US28214.
PR   30-NOV-1999;   99WO-US28313.
PR   30-NOV-1999;   99WO-US28409.
PR   01-DEC-1999;   99WO-US28301.
PR   01-DEC-1999;   99WO-US28634.
PR   02-DEC-1999;   99WO-US28551.
PR   02-DEC-1999;   99WO-US28564.
PR   02-DEC-1999;   99WO-US28565.
PR   16-DEC-1999;   99WO-US30095.
PR   20-DEC-1999;   99WO-US30911.
PR   20-DEC-1999;   99WO-US30999.
PR   22-DEC-1999;   99WO-US30720.
PR   30-DEC-1999;   99WO-US31243.
PR   30-DEC-1999;   99WO-US31274.
PR   05-JAN-2000;  2000WO-US00219.
PR   06-JAN-2000;  2000WO-US00277.
PR   06-JAN-2000;  2000WO-US00376.
PR   11-FEB-2000;  2000WO-US03565.
PR   18-FEB-2000;  2000WO-US04341.
PR   18-FEB-2000;  2000WO-US04342.
PR   22-FEB-2000;  2000WO-US04414.
PR   24-FEB-2000;  2000WO-US04914.
PR   24-FEB-2000;  2000WO-US05004.
PR   01-MAR-2000;  2000WO-US05601.
PR   02-MAR-2000;  2000WO-US05746.
PR   02-MAR-2000;  2000WO-US05841.
PR   10-MAR-2000;  2000WO-US06319.
PR   15-MAR-2000;  2000WO-US06884.
PR   20-MAR-2000;  2000WO-US07377.
PR   21-MAR-2000;  2000WO-US07532.
PR   30-MAR-2000;  2000WO-US08439.
PR   17-MAY-2000;  2000WO-US13705.
PR   22-MAY-2000;  2000WO-US14042.
PR   30-MAY-2000;  2000WO-US14941.
PR   02-JUN-2000;  2000WO-US15264.
PR   28-JUL-2000;  2000WO-US20710.
PR   11-AUG-2000;  2000WO-US22031.
PR   23-AUG-2000;  2000WO-US23522.
PR   24-AUG-2000;  2000WO-US23328.
PR   08-NOV-2000;  2000WO-US30952.
PR   10-NOV-2000;  2000WO-US30873.
PR   01-DEC-2000;  2000WO-US32678.
PR   20-DEC-2000;  2000WO-US34956.
PR   28-FEB-2001;  2001WO-US06520.
PR   01-MAR-2001;  2001WO-US06666.
PR   25-MAY-2001;  2001WO-US17092.
PR   01-JUN-2001;  2001WO-US17800.
PR   20-JUN-2001;  2001WO-US19692.
PR   22-JUN-2001;  2001WO-US20116.
PR   29-JUN-2001;  2001WO-US21066.
PR   09-JUL-2001;  2001WO-US21735.
PR   20-DEC-2000;  2000US-0747259.
PR   28-FEB-2001;  2001US-0796498.
PR   09-MAR-2001;  2001US-0802706.
PR   14-MAR-2001;  2001US-0808689.
PR   22-MAR-2001;  2001US-0816744.
PR   05-APR-2001;  2001US-0828366.
PR   10-MAY-2001;  2001US-0854208.
```

```
Qy        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240

Qy        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300

Qy        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
              |||||||||||||||||||||||||||||||||||||||||||
Db        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344


RESULT 8
ABU72061
ID   ABU72061 standard; Protein; 344 AA.
XX
AC   ABU72061;
XX
DT   11-JUN-2003  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO337.
XX
KW   Human; secreted and transmembrane polypeptide; PRO;
KW   fibroblast growth factor receptor; PRO533; PRO301; PRO187; PRO337;
KW   PRO1411; PRO10096; PRO246; PRO6307; PRO6003; FGFR-3; FGFR-4; FGFR-1;
KW   FGFR-2; PRO6004; PRO4356; PRO2630; PRO265; PRO951; bioactive molecule;
KW   toxin; radiolabel; antibody; cell death; chromosome mapping;
KW   gene mapping; transgenic animal; knockout animal; gene therapy;
KW   tissue typing.
XX
OS   Homo sapiens.
XX
PN   US2002177165-A1.
XX
PD   28-NOV-2002.
XX
PF   01-FEB-2002; 2002US-0066500.
XX
PR   14-JUL-1998;   98WO-US14552.
PR   10-SEP-1998;   98WO-US18824.
PR   14-SEP-1998;   98WO-US19093.
PR   16-SEP-1998;   98WO-US19330.
PR   17-SEP-1998;   98WO-US19437.
PR   20-NOV-1998;   98WO-US24855.
PR   25-NOV-1998;   98WO-US25190.
PR   01-DEC-1998;   98WO-US25108.
PR   08-MAR-1999;   99WO-US05028.
PR   02-JUN-1999;   99WO-US12252.
PR   01-SEP-1999;   99WO-US20111.
PR   08-SEP-1999;   99WO-US20594.
PR   15-SEP-1999;   99WO-US21090.
PR   15-SEP-1999;   99WO-US21547.
PR   30-NOV-1999;   99WO-US28313.
PR   01-DEC-1999;   99WO-US28301.
PR   02-DEC-1999;   99WO-US28565.
PR   20-DEC-1999;   99WO-US30999.
PR   05-JAN-2000; 2000WO-US00219.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   22-FEB-2000; 2000WO-US04414.
PR   01-MAR-2000; 2000WO-US05601.
PR   02-MAR-2000; 2000WO-US05841.
PR   09-MAR-2000; 2000WO-US06471.
PR   20-MAR-2000; 2000WO-US07377.
PR   30-MAR-2000; 2000WO-US08439.
PR   15-MAY-2000; 2000WO-US13358.
PR   17-MAY-2000; 2000WO-US13705.
PR   22-MAY-2000; 2000WO-US14042.
PR   30-MAY-2000; 2000WO-US14941.
PR   02-JUN-2000; 2000WO-US15264.
PR   11-AUG-2000; 2000WO-US22031.
PR   23-AUG-2000; 2000WO-US23522.
PR   24-AUG-2000; 2000WO-US23328.
PR   01-DEC-2000; 2000WO-US32678.
PR   28-FEB-2001; 2001WO-US06520.
PR   30-MAY-2001; 2001WO-US17443.
PR   01-JUN-2001; 2001WO-US17800.
PR   20-JUN-2001; 2001WO-US19692.
PR   29-JUN-2001; 2001WO-US21066.
PR   09-JUL-2001; 2001WO-US21735.
PR   26-AUG-1997;   97US-056974P.
PR   17-SEP-1997;   97US-059115P.
PR   18-SEP-1997;   97US-059263P.
PR   19-SEP-1997;   97US-059588P.
PR   17-OCT-1997;   97US-062285P.
PR   24-OCT-1997;   97US-062816P.
PR   24-OCT-1997;   97US-063082P.
PR   27-OCT-1997;   97US-063329P.
PR   29-OCT-1997;   97US-063733P.
PR   21-NOV-1997;   97US-066364P.
PR   25-NOV-1997;   97US-066840P.
PR   16-DEC-1997;   97US-069694P.
PR   09-FEB-1998;   98US-074086P.
PR   09-FEB-1998;   98US-074092P.
PR   25-MAR-1998;   98US-079294P.
PR   08-APR-1998;   98US-081049P.
PR   10-AUG-1998;   98US-095998P.
PR   18-AUG-1998;   98US-097000P.
PR   09-SEP-1998;   98US-099601P.
PR   10-SEP-1998;   98US-099803P.
PR   10-SEP-1998;   98US-099811P.
PR   10-SEP-1998;   98US-099812P.
PR   17-SEP-1998;   98US-100858P.
PR   24-SEP-1998;   98US-101922P.
PR   28-OCT-1998;   98US-106032P.
PR   20-NOV-1998;   98US-109304P.
PR   23-MAR-1999;   99US-125778P.
PR   15-JUN-1999;   99US-139695P.
PR   20-JUL-1999;   99US-145070P.
PR   26-JUL-1999;   99US-145698P.
PR   17-AUG-1999;   99US-149396P.
PR   07-DEC-1999;   99US-169495P.
PR   15-NOV-2001; 2001US-0002796.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Botstein DA,  Desnoyers L,  Eaton DL;
PI   Ferrara N,  Fong S,  Gao W,  Gerber H,  Gerritsen ME,  Goddard A;
PI   Godowski PJ,  Gurney AL,  Kljavin IJ,  Mather JP,  Napier MA,  Pan J;
PI   Paoni NF,  Roy MA,  Stewart TA,  Tumas D,  Watanabe CK,  Williams PM;
PI   Wood WI,  Zhang Z;
XX
DR   WPI; 2003-328482/31.
DR   N-PSDB; ACA60526.
XX
PT   Novel secreted and transmembrane polypeptide for modulating biological
PT   activity of cell expressing the polypeptide, for identifying agonists
PT   or antagonists of polypeptide, and as molecular weight markers -
XX
PS   Claim 12; Fig 52; 254pp; English.
XX
CC   The invention describes an isolated, secreted and transmembrane
CC   polypeptide (PP), termed PRO PP or fibroblast growth factor receptor PP
CC   (I). (I) is useful for detecting PRO533, PRO301, PRO187, PRO337,
CC   PRO1411, PRO10096, PRO246, PRO6307, PRO6003, fibroblast growth factor
CC   receptor (FGFR)-3, FGFR-4, FGFR-1, FGFR-2, PRO6004, PRO4356, PRO2630,
CC   PRO265 or PRO951 polypeptide, and for linking a bioactive molecule to a
CC   cell expressing the above polypeptides. The bioactive molecule, a toxin,
CC   radiolabel or an antibody, causes cell death. PRO is useful in assays to
CC   identify other proteins or molecules involved in binding interaction.
CC   The polynucleotide (II) encoding (I) is useful in chromosome and gene
CC   mapping, in generation of antisense RNA and DNA, for generating
CC   transgenic animals or knockout animals which in turn are useful in the
CC   development and screening of therapeutically useful reagents, to
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```
PT   One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT   useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT   infarction), endothelial or angiogenic disorders in a mammal -
XX
PS   Claim 11; Fig 56; 565pp; English.
XX
CC   ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC   ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
CC   antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
CC   activities, and can be used in gene therapy. The PRO polynucleotides,
CC   proteins, agonists and antagonists are useful for treating or diagnosing
CC   a cardiovascular, endothelial or angiogenic disorder in a mammal,
CC   e.g. cardiac hypertrophy, trauma, cancer, age-related macular
CC   degeneration, atherosclerosis, hypertension, arterial restenosis,
CC   rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
CC   lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
CC   carcinoma) and wound healing. The PRO polynucleotides have applications
CC   in molecular biology, including use as hybridisation probes, and in
CC   chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
CC   probes used in the exemplification of the present invention.
XX
SQ   Sequence   344 AA;

  Query Match           100.0%;  Score 1806;  DB 23;  Length 344;
  Best Local Similarity  100.0%;  Pred. No. 3e-149;
  Matches  344;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60

Qy         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120

Qy        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180

Qy        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240

Qy        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300

Qy        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
              |||||||||||||||||||||||||||||||||||||||||||
Db        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344


RESULT 7
AAU83654
ID   AAU83654 standard; Protein; 344 AA.
XX
AC   AAU83654;
XX
DT   08-MAY-2002  (first entry)
XX
DE   Human PRO protein, Seq ID No 126.
XX
KW   Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW   breast cancer; prostate tumour; rectal tumour; liver tumour;
KW   pericyte cell proliferation; chondrocyte cell proliferation;
KW   tumour necrosis factor-alpha.
XX
OS   Homo sapiens.
XX
PN   WO200208288-A2.
XX
PD   31-JAN-2002.
XX
PF   29-JUN-2001; 2001WO-US21066.
XX
PR   20-JUL-2000; 2000US-219556P.
PR   25-JUL-2000; 2000US-220585P.
PR   25-JUL-2000; 2000US-220605P.
PR   25-JUL-2000; 2000US-220607P.
PR   25-JUL-2000; 2000US-220624P.
PR   25-JUL-2000; 2000US-220638P.
PR   25-JUL-2000; 2000US-220664P.
PR   25-JUL-2000; 2000US-220666P.
PR   26-JUL-2000; 2000US-220893P.
PR   28-JUL-2000; 2000WO-US20710.
PR   23-AUG-2000; 2000WO-US23522.
PR   24-AUG-2000; 2000WO-US23328.
PR   15-SEP-2000; 2000US-000000P.
PR   10-NOV-2000; 2000WO-US30873.
PR   28-NOV-2000; 2000US-253646P.
PR   01-DEC-2000; 2000WO-US32678.
PR   20-DEC-2000; 2000US-0747259.
PR   20-DEC-2000; 2000WO-US34956.
PR   28-FEB-2001; 2001WO-US06520.
PR   10-MAY-2001; 2001US-0854280.
PR   25-MAY-2001; 2001WO-US17092.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Desnoyers L,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi JC,  Gurney AL,  Smith V,  Stephan JF,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2002-172001/22.
DR   N-PSDB; ABK33598.
XX
PT   One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT   useful for treating a PRO related disorder and for diagnosing tumours
PT   such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
PT   tumour or liver tumour -
XX
PS   Claim 11; Figure 126; 359pp; English.
XX
CC   The invention relates to one hundred and twenty two nucleic acids
CC   encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
CC   encode human secreted proteins. The PRO nucleic acids, polypeptides,
CC   agonists and antagonists are useful for treating a PRO related disorder.
CC   The PRO polypeptides are useful for diagnosing tumours, especially lung
CC   cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
CC   liver tumour. The PRO polypeptides are useful for stimulating the
CC   proliferation of, or gene expression, in pericyte cells, for stimulating
CC   the proliferation or differentiation of chondrocyte cells, for
CC   stimulating the release of tumour necrosis factor-alpha from human blood,
CC   for stimulating or inhibiting the proliferation of normal human dermal
CC   fibroblast cells. The PRO polypeptide may also be used as molecular
CC   weight markers and for tissue typing. The PRO nucleic acids have
CC   applications in molecular biology, including use as hybridisation probes,
CC   and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
CC   protein sequences of the invention.
XX
SQ   Sequence   344 AA;

  Query Match           100.0%;  Score 1806;  DB 23;  Length 344;
  Best Local Similarity  100.0%;  Pred. No. 3e-149;
  Matches  344;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60

Qy         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120

Qy        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180
```

PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 28-JUN-2001; 2001WO-US00000.
XX
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR WPI; 2002-171999/22.
DR N-PSDB; ABL95588.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal
XX
PS Claim 11; Fig 56; 567pp; English.
XX
CC The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a PRO protein of the invention.
XX
SQ Sequence 344 AA;

Query Match 100.0%; Score 1806; DB 23; Length 344;
Best Local Similarity 100.0%; Pred. No. 3e-149;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60

Qy         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120

Qy        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180

Qy        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240

Qy        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300

Qy        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
              |||||||||||||||||||||||||||||||||||||||||||
Db        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
```

RESULT 6
ABB84844
ID ABB84844 standard; Protein; 344 AA.
XX
AC ABB84844;
XX
DT 16-MAY-2002 (first entry)
XX
DE Human PRO337 protein sequence SEQ ID NO:56.
XX
KW Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
KW vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW age-related macular degeneration; arterial restenosis; angina;
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW wound healing; chromosome mapping; gene mapping.
XX
OS Homo sapiens.
XX
PN WO200200690-A2.
XX
PD 03-JAN-2002.
XX
PF 20-JUN-2001; 2001WO-US19692.
XX
PR 23-JUN-2000; 2000US-213637P.
PR 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220664P.
PR 28-JUL-2000; 2000WO-US20710.
PR 02-AUG-2000; 2000US-222695P.
PR 17-AUG-2000; 2000US-0643657.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 07-SEP-2000; 2000US-230978P.
PR 18-SEP-2000; 2000US-0664610.
PR 18-SEP-2000; 2000US-0665350.
PR 24-OCT-2000; 2000US-242922P.
PR 08-NOV-2000; 2000US-0709238.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 22-JAN-2001; 2001US-0767609.
PR 28-FEB-2001; 2001US-0796498.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 25-MAY-2001; 2001WO-US17092.
PR 30-MAY-2001; 2001US-0870574.
PR 30-MAY-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR WPI; 2002-090516/12.
DR N-PSDB; ABL88099.
XX

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XX
PR   15-JUN-1999;   99US-0139695.
PR   20-JUL-1999;   99US-0145070.
PR   26-JUL-1999;   99US-0145698.
PR   17-AUG-1999;   99US-0149396.
PR   01-SEP-1999;   99WO-US20111.
PR   08-SEP-1999;   99WO-US20594.
PR   15-SEP-1999;   99WO-US21090.
PR   15-SEP-1999;   99WO-US21547.
PR   30-NOV-1999;   99WO-US28313.
PR   01-DEC-1999;   99WO-US28301.
PR   02-DEC-1999;   99WO-US28565.
PR   07-DEC-1999;   99US-0169495.
PR   05-JAN-2000; 2000WO-US00219.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   22-FEB-2000; 2000WO-US04414.
PR   01-MAR-2000; 2000WO-US05601.
PR   02-MAR-2000; 2000WO-US05841.
PR   20-MAR-2000; 2000WO-US07377.
PR   30-MAR-2000; 2000WO-US08439.
PR   15-MAY-2000; 2000WO-US13358.
PR   17-MAY-2000; 2000WO-US13705.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Botstein DA,  Desnoyers L,  Eaton DL;
PI   Ferrara N,  Fong S,  Gao W,  Gerber H,  Gerritsen ME,  Goddard A;
PI   Godowski PJ,  Gurney AL,  Kljavin IJ,  Mather JP,  Napier MA,  Pan J;
PI   Paoni NF,  Roy MA,  Stewart TA,  Tumas D,  Watanabe CK,  Williams PM;
PI   Wood WI,  Zhang Z;
XX
DR   WPI; 2001-050091/06.
DR   N-PSDB; AAC87037.
XX
PT   Isolated nucleic acid molecule encoding a PRO polypeptide which is a
PT   transmembrane polypeptide is useful for gene therapy and identification
PT   of related polypeptides -
XX
PS   Claim 12; Fig 52; 244pp; English.
XX
CC   The present sequence represents a human secreted and transmembrane
CC   polypeptide. The specification describes human polypeptides, designated
CC   PRO196, PRO444, PRO183, PRO185, PRO210, PRO215, PRO217, PRO242, PRO288,
CC   PRO365, PRO1361, PRO1308, PRO1183, PRO1272, PRO1419, PRO4999, PRO7170,
CC   PRO248, PRO353, PRO1318, PRO1600, PRO9940, PRO533, PRO301, PRO187,
CC   PRO337, PRO1411, PRO4356, PRO246, PRO265, PRO941, PRO10096, PRO6003,
CC   PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of cells
CC   can be modulated with agents that bind to these polypeptides, resulting
CC   in the death of the cells. The polynucleotides encoding these
CC   polypeptides are useful in the recombinant production of the
CC   polypeptides, as a hybridisation probe to screen libraries to isolate
CC   homologous sequences, or to map the gene. They may also be used for
CC   analysing genetic disorders, and to produce transgenic animals which are
CC   useful for the development and screening of therapeutically useful
CC   reagents. The polynucleotides can also be used in gene therapy e.g. to
CC   replace a defective gene.
XX
SQ   Sequence   344 AA;

  Query Match           100.0%;  Score 1806;  DB 22;  Length 344;
  Best Local Similarity  100.0%;  Pred. No. 3e-149;
  Matches  344;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60

Qy         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120

Qy        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180

Qy        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240

Qy        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300

Qy        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
              |||||||||||||||||||||||||||||||||||||||||||||
Db        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344


RESULT 5
ABB95450
ID   ABB95450 standard; Protein; 344 AA.
XX
AC   ABB95450;
XX
DT   19-JUL-2002  (first entry)
XX
DE   Human angiogenesis related protein PRO337 SEQ ID NO: 56.
XX
KW   Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW   atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW   cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;
KW   antiarteriosclerotic.
XX
OS   Homo sapiens.
XX
PN   WO200208284-A2.
XX
PD   31-JAN-2002.
XX
PF   09-JUL-2001; 2001WO-US21735.
XX
PR   20-JUL-2000; 2000US-219556P.
PR   25-JUL-2000; 2000US-220624P.
PR   25-JUL-2000; 2000US-220664P.
PR   28-JUL-2000; 2000WO-US20710.
PR   02-AUG-2000; 2000US-222695P.
PR   17-AUG-2000; 2000US-0643657.
PR   23-AUG-2000; 2000WO-US23522.
PR   24-AUG-2000; 2000WO-US23328.
PR   07-SEP-2000; 2000US-230978P.
PR   15-SEP-2000; 2000US-000000P.
PR   18-SEP-2000; 2000US-0664610.
PR   18-SEP-2000; 2000US-0665350.
PR   24-OCT-2000; 2000US-242922P.
PR   08-NOV-2000; 2000US-0709238.
PR   08-NOV-2000; 2000WO-US30952.
PR   10-NOV-2000; 2000WO-US30873.
PR   01-DEC-2000; 2000WO-US32678.
PR   20-DEC-2000; 2000US-0747259.
PR   20-DEC-2000; 2000WO-US34956.
PR   22-JAN-2001; 2001US-0767609.
PR   28-FEB-2001; 2001US-0796498.
PR   28-FEB-2001; 2001WO-US06520.
PR   01-MAR-2001; 2001WO-US06666.
PR   09-MAR-2001; 2001US-0802706.
PR   14-MAR-2001; 2001US-0808689.
PR   22-MAR-2001; 2001US-0816744.
PR   05-APR-2001; 2001US-0828366.
PR   10-MAY-2001; 2001US-0854208.
PR   10-MAY-2001; 2001US-0854280.
PR   25-MAY-2001; 2001US-0866028.
PR   25-MAY-2001; 2001US-0866034.
PR   25-MAY-2001; 2001WO-US17092.
PR   30-MAY-2001; 2001US-0870574.
PR   30-MAY-2001; 2001WO-US17443.
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```
AAU12359
ID   AAU12359 standard; Protein; 344 AA.
XX
AC   AAU12359;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human PRO337 polypeptide sequence.
XX
KW   Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW   breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW   cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KW   adipocyte; A-peptide; factor VIIA; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200140466-A2.
XX
PD   07-JUN-2001.
XX
PF   01-DEC-2000; 2000WO-US32678.
XX
PR   01-DEC-1999;   99WO-US28301.
PR   01-DEC-1999;   99WO-US28634.
PR   02-DEC-1999;   99WO-US28551.
PR   02-DEC-1999;   99WO-US28564.
PR   02-DEC-1999;   99WO-US28565.
PR   09-DEC-1999;   99US-0170262.
PR   16-DEC-1999;   99WO-US30095.
PR   20-DEC-1999;   99WO-US30911.
PR   20-DEC-1999;   99WO-US30999.
PR   30-DEC-1999;   99WO-US31243.
PR   06-JAN-2000;  2000WO-US00277.
PR   06-JAN-2000;  2000WO-US00376.
PR   11-FEB-2000;  2000WO-US03565.
PR   18-FEB-2000;  2000WO-US04341.
PR   18-FEB-2000;  2000WO-US04342.
PR   22-FEB-2000;  2000WO-US04414.
PR   24-FEB-2000;  2000WO-US04914.
PR   24-FEB-2000;  2000WO-US05004.
PR   01-MAR-2000;  2000WO-US05601.
PR   20-MAR-2000;  2000WO-US07377.
PR   21-MAR-2000;  2000WO-US07532.
PR   30-MAR-2000;  2000WO-US08439.
PR   17-MAY-2000;  2000WO-US13705.
PR   22-MAY-2000;  2000WO-US14042.
PR   30-MAY-2000;  2000WO-US14941.
PR   02-JUN-2000;  2000WO-US15264.
PR   10-NOV-2000;  2000WO-US30873.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Beresini M,  Deforge L,  Desnoyers L,  Filvaroff E,  Gao W;
PI   Gerritsen ME,  Goddard A,  Godowski PJ,  Gurney AL,  Sherwood S;
PI   Smith V,  Stewart TA,  Tumas D,  Watanabe CK,  Wood WI,  Zhang Z;
XX
DR   WPI; 2001-408281/43.
DR   N-PSDB; AAS21431.
XX
PT   Isolated, secretory and transmembrane PRO polypeptide used to detect
PT   other PRO polypeptides, link bioactive molecules to cells expressing
PT   PRO polypeptides, and detect the presence of mammalian tumours e.g.
PT   lung, breast, prostate, cervical
XX
PS   Claim 12; Fig 376; 813pp; English.
XX
CC   AAU12172-AAU12446 represent novel human secretory and transmembrane
CC   PRO polypeptides. The PRO polypeptides are useful to detect other
CC   PRO polypeptides, to link bioactive molecules to cells expressing
CC   PRO polypeptides, to modulate biological activities of cells expressing
CC   PRO polypeptides, and to detect the presence of mammalian lung, colon,
CC   breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC   polypeptide expression in a cell sample to that in a control sample.
CC   Some of the 275 sequences are also useful to stimulate the release of
CC   tumour necrosis factor-alpha (TNF-alpha) from human blood, the
CC   proliferation or differentiation of chondrocytes, the proliferation or
CC   gene expression in pericyte cells, the release of proteoglycans from
CC   cartilage, the proliferation of inner ear utricular supporting cells or
CC   of T-lymphocytes, the release of a cytokine from peripheral blood
CC   monocytes (PBMCs), or the proliferation of endothelial cells. Some of
CC   the PRO polypeptides may modulate glucose or free fatty acid uptake by
CC   skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
CC   to factor VIIA. The PRO polypeptides can be used in assays to identify
CC   molecules involved in binding interactions. The polynucleotides encoding
CC   PRO polypeptides can be used to generate probes, antisense RNA/DNA,
CC   transgenic or knock out animals and can be used in gene therapy.
XX
SQ   Sequence  344 AA;

  Query Match           100.0%;  Score 1806;  DB 22;  Length 344;
  Best Local Similarity  100.0%;  Pred. No. 3e-149;
  Matches  344;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60

Qy         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120

Qy        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180

Qy        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240

Qy        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300

Qy        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
              |||||||||||||||||||||||||||||||||||||||||||
Db        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344


RESULT 4
AAB31204
ID   AAB31204 standard; Protein; 344 AA.
XX
AC   AAB31204;
XX
DT   20-APR-2001  (first entry)
XX
DE   Amino acid sequence of human polypeptide PRO337.
XX
KW   Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;
KW   PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO1308;
KW   PRO1183; PRO1272; PRO1419; PRO4999; PRO7170; PRO248; PRO353; PRO1318;
KW   PRO1600; PRO9940; PRO533; PRO301; PRO187; PRO337; PRO1411; PRO4356;
KW   PRO246; PRO265; PRO941; PRO10096; PRO6003; PRO6004; PRO350; PRO2630;
KW   PRO6309; cell death; genetic disorder; transgenic animal; gene therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..28
FT                   /note= "signal peptide"
XX
PN   WO200077037-A2.
XX
PD   21-DEC-2000.
XX
PF   22-MAY-2000; 2000WO-US14042.
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PR   02-DEC-1999;   99WO-US28565.
PR   16-DEC-1999;   99WO-US30095.
PR   30-DEC-1999;   99WO-US31243.
PR   30-DEC-1999;   99WO-US31274.
PR   05-JAN-2000;  2000WO-US00219.
PR   06-JAN-2000;  2000WO-US00277.
PR   06-JAN-2000;  2000WO-US00376.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Botstein D,  Desnoyers L,  Eaton DL;
PI   Ferrara N,  Filvaroff E,  Fong S,  Gao W,  Gerber H,  Gerritsen ME;
PI   Goddard A,  Godowski PJ,  Grimaldi CJ;  Gurney AL,  Hillan KJ;
PI   Kljavin IJ,  Kuo SS,  Napier MA,  Pan J,  Paoni NF,  Roy MA;
PI   Shelton DL,  Stewart TA,  Tumas D,  Williams PM,  Wood WI;
XX
DR   WPI; 2000-611443/58.
DR   N-PSDB; AAC78590.
XX
PT   Novel PRO polypeptides and polynucleotides used in detection methods,
PT   to target bioactive molecules to specific cells, and to modulate
PT   cellular activities -
XX
PS   Claim 12; Fig 222; 636pp; English.
XX
CC   AAC78458 to AAC78599 represent polynucleotide and EST (expressed
CC   sequence tag) sequences which encode secreted or transmembrane PRO
CC   polypeptides. The PRO polynucleotides and polypeptides have cytostatic
CC   activity. The polynucleotides and polypeptides can be used for detecting
CC   the presence of PRO polypeptides in samples, for linking bioactive
CC   molecules to cells and for modulating biological activities of cells,
CC   using the polypeptides for specific targeting. The polypeptide targeting
CC   can be used to kill the target cells, e.g. for the treatment of cancers.
CC   The polypeptide pairs provide specific targeting of bioactive molecules
CC   to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
CC   the isolation of the PRO polynucleotide sequences.
XX
SQ   Sequence   344 AA;

  Query Match          100.0%;  Score 1806;  DB 21;  Length 344;
  Best Local Similarity   100.0%;  Pred. No. 3e-149;
  Matches  344;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60

Qy         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120

Qy        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180

Qy        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240

Qy        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300

Qy        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
              |||||||||||||||||||||||||||||||||||||||||||||
Db        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344


RESULT 2
AAY57601
ID   AAY57601 standard; Protein; 344 AA.
XX
AC   AAY57601;
XX
DT   10-MAR-2000  (first entry)
XX
DE   Human protein SEQ ID NO:1.
XX
KW   Human; haematopoietic cell regulation; tissue generation; reparation;
KW   activin; inhibin; taxis; chemotaxis; blood coagulation; thrombus;
KW   receptor; ligand; autoimmune; infection-related immunodeficiency;
KW   inflammatory disorder; neurological disease.
XX
OS   Homo sapiens.
XX
PN   WO9958668-A1.
XX
PD   18-NOV-1999.
XX
PF   13-MAY-1999;   99WO-JP02485.
XX
PR   14-MAY-1998;   98JP-0131815.
XX
PA   (ONOY ) ONO PHARM CO LTD.
XX
PI   Fukushima D,  Shibayama S,  Tada H;
XX
DR   WPI; 2000-062298/05.
DR   N-PSDB; AAZ47892, AAZ47893.
XX
PT   New polypeptides of human origin having cell regulatory, tissue
PT   generation, coagulant and other activities -
XX
PS   Claim 1; Page 38-40; 84pp; Japanese.
XX
CC   The present sequence represents a specifically claimed novel human
CC   protein. The novel human protein can be used in therapeutic drugs for
CC   the prevention and treatment of a broad range of disorders including
CC   autoimmune and infection-related immunodeficiency, inflammatory
CC   disorders, and neurological diseases. The novel protein is expected of
CC   having haematopoietic cell regulatory activity, tissue generation/
CC   reparation activity, activin/inhibin activity, taxis/chemotaxis activity,
CC   blood coagulation and thrombus activity, and receptor/ligand activity.
XX
SQ   Sequence   344 AA;

  Query Match          100.0%;  Score 1806;  DB 21;  Length 344;
  Best Local Similarity   100.0%;  Pred. No. 3e-149;
  Matches  344;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60

Qy         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120

Qy        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180
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Db        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180

Qy        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240
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Db        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240

Qy        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300
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Db        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300

Qy        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
              |||||||||||||||||||||||||||||||||||||||||||||
Db        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344


RESULT 3
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 11, 2003, 02:49:08 ; Search time 72 Seconds
(without alignments)
758.360 Million cell updates/sec

Title: US-10-017-084A-523
Perfect score: 1806
Sequence: 1 MKTIQPKMHNSISWAIFTGL.....RRAGCVWLLPLLVLHLLLKF 344

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1806	100.0	344	21	AAB44329	Human PRO337 prote
2	1806	100.0	344	21	AAY57601	Human protein SEQ
3	1806	100.0	344	22	AAU12359	Human PRO337 polyp
4	1806	100.0	344	22	AAB31204	Amino acid sequenc
5	1806	100.0	344	23	ABB95450	Human angiogenesis
6	1806	100.0	344	23	ABB84844	Human PRO337 prote
7	1806	100.0	344	23	AAU83654	Human PRO protein,
8	1806	100.0	344	24	ABU72061	Novel human secret
9	1806	100.0	344	24	ABU66757	Human PRO polypept
10	1806	100.0	344	24	ABU67033	Human secreted/tra
11	1806	100.0	344	24	ABU67162	Novel human secret
12	1806	100.0	344	24	ABU67293	Novel human secret
13	1806	100.0	344	24	ABU59838	Novel secreted and
14	1806	100.0	344	24	ABU61159	Human PRO337 polyp
15	1806	100.0	355	22	AAM40499	Human polypeptide
16	1799	99.6	344	21	AAB19721	Human SECX Clone 1
17	1799	99.6	344	21	AAB19722	Human SECX Clone 1
18	1791.5	99.2	343	20	AAY41773	Human PRO337 prote
19	1665.5	92.2	344	22	AAM38713	Human polypeptide
20	1665.5	92.2	344	24	ABU56719	Lung cancer-associ
21	1643	91.0	381	23	AAU79205	Human Kruppel asso
22	1642	90.9	313	21	AAY57602	Human protein SEQ
23	932.5	51.6	335	23	AAO19641	Human limbic syste
24	926.5	51.3	338	17	AAW05153	Rat LAMP residues
25	926.5	51.3	338	17	AAW05154	Rat LAMP residues
26	923.5	51.1	325	17	AAW05152	Human LAMP residue
27	913	50.6	361	17	AAW05172	Rat LAMP clone 6c.
28	908	50.3	308	17	AAW05157	Human LAMP residue
29	907	50.2	315	17	AAW05158	Rat LAMP residues
30	905	50.1	310	17	AAW05156	Rat mature LAMP.
31	902	49.9	304	17	AAW05155	Human mature LAMP.
32	893	49.4	383	24	ABR39441	Human GENSET polyp
33	886.5	49.1	287	17	AAW05159	Human LAMP residue
34	885.5	49.0	287	17	AAW05160	Rat LAMP residues
35	852.5	47.2	326	22	AAG75020	Human colon cancer
36	823	45.6	354	22	AAB31212	Amino acid sequenc
37	823	45.6	354	23	ABP53580	Human NOV12a prote
38	823	45.6	354	23	AAU83592	Human PRO protein,
39	823	45.6	354	24	ABU72069	Novel human secret
40	823	45.6	354	24	ABU67170	Novel human secret
41	823	45.6	354	24	ABU67301	Novel human secret
42	822	45.5	354	23	ABB98407	Human NOV6, KILON-
43	819	45.3	354	23	ABP53581	Human NOV12b prote
44	815	45.1	352	21	AAB44331	Human PRO4993 prot
45	815	45.1	352	24	ABU61161	Human PRO4993 poly

ALIGNMENTS

RESULT 1
AAB44329
ID AAB44329 standard; Protein; 344 AA.
XX
AC AAB44329;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human PRO337 protein sequence SEQ ID NO:523.
XX
KW Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
KW expressed sequence tag; detection; cancer.
XX
OS Homo sapiens.
XX
PN WO200053756-A2.
XX
PD 14-SEP-2000.
XX
PF 18-FEB-2000; 2000WO-US04341.
XX
PR 08-MAR-1999; 99WO-US05028.
PR 12-MAR-1999; 99US-0123957.
PR 29-MAR-1999; 99US-0126773.
PR 21-APR-1999; 99US-0130232.
PR 28-APR-1999; 99US-0131445.
PR 14-MAY-1999; 99US-0134287.
PR 23-JUN-1999; 99US-0141037.
PR 26-JUL-1999; 99US-0145698.
PR 29-OCT-1999; 99US-0162506.
PR 30-NOV-1999; 99WO-US28313.
PR 02-DEC-1999; 99WO-US28551.

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Qy       721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAA 780
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Db       721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAA 780

Qy       781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840
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Db       781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840

Qy       841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900
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Db       841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900

Qy       901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960
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Db       901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960

Qy       961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020
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Db      1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080

Qy      1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140
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Qy      1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200
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Db      1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200

Qy      1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
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Search completed: September 11, 2003, 03:01:23
Job time : 573 secs

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16/1
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$52.47 27527509229

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300
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Qy        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
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Db        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600

Qy        601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660
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Qy        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
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Db        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
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Qy       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
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Db       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320

Qy       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380
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Db       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380

Qy       1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440
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Qy       1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500
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Qy       1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620
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Qy       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
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RESULT 15
US-09-978-423A-522
; Sequence 522, Application US/09978423A
; Publication No. US20030069178A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C21
; CURRENT APPLICATION NUMBER: US/09/978,423A
; CURRENT FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086023

Query Match 100.0%; Score 1679; DB 11; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60

Qy         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120
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Qy        121 AAGAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180
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Db        121 AAGAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180

Qy        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240
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Db        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240

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Qy        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
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Db        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360

Qy        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420
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Db        601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660

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Db        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720

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Db        721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCCGTGGTACGGAGAGTAAA 780

Qy        781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840
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Qy        901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960
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Qy        961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020
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Db        961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020

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Db       1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140
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RESULT 14
US-09-918-585A-522
; Sequence 522, Application US/09918585A
; Publication No. US20030060406A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C1
; CURRENT APPLICATION NUMBER: US/09/918,585A
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1679; DB 11; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60
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Db          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60

Qy         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120
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Qy        121 AAGAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180
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Db        121 AAGAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180

Qy        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240
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Qy        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
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Db        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360

Qy        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420
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Db        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420

Qy        421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
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Qy        481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540
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Qy        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
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Db        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600

Qy        601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660
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Db        601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660

Qy        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
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Db        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720

Qy        721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCCGTGGTACGGAGAGTAAA 780
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Db        721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCCGTGGTACGGAGAGTAAA 780

Qy        781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840
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Db        781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840

Qy        841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900
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Qy        901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960
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Db        901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960

Qy        961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020
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Qy       1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080
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Db       1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080

Qy       1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140
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Db       1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140

Qy       1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200

Qy       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
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Db       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260

Qy       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320
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Db       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320

Qy       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380
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Db       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380

Qy       1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440
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Db       1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440

Qy       1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C14
; CURRENT APPLICATION NUMBER: US/09/978,824
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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;  PRIOR APPLICATION NUMBER: 60/085573
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;  PRIOR APPLICATION NUMBER: 60/085704
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/085697

  Query Match           100.0%;  Score 1679;  DB 11;  Length 1679;
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  Matches 1679;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60
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Db          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60

Qy         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120
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Qy        121 AAGAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180
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Db        121 AAGAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180

Qy        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240
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Db        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240

Qy        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
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Qy        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420
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Qy        481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540
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Db        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720

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Db        721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCCGTGGTACGGAGAGTAAA 780

Qy        781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840
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Db        781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840

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Qy       1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080
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Qy       1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140
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Qy       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
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Db       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260

Qy       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320
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RESULT 13
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; Sequence 522, Application US/09978824
; Publication No. US20030055216A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
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; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
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; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
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RESULT 12
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; Sequence 522, Application US/09981915A
; Publication No. US20030054986A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C12
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; CURRENT FILING DATE: 2001-10-16
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1679; DB 11; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620

Qy       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAAGAGCAAAAAAAAA 1679
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RESULT 11
US-09-999-833A-522
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; Sequence 522, Application US/09999833A
; Publication No. US20030054405A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C65
;  CURRENT APPLICATION NUMBER: US/09/999,833A
;  CURRENT FILING DATE:  2001-10-24
;  PRIOR APPLICATION NUMBER: 09/918585
;  PRIOR FILING DATE: 2001-07-30
;  PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1679; DB 11; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60
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Db          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60

Qy         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAAGAAGAAAAAGAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAAGAAGAAAAAGAAG 120

Qy        121 AAGAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180

Qy        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240
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Db        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240

Qy        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCCACCCTCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300

Qy        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
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Qy        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420
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Db        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420

Qy        421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
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Db        421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480

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Qy       1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200
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Db       1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200

Qy       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
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Db       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260

Qy       1261 TATACAAATGAAATTAGAACAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320
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Db       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320

Qy       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380
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Db       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380

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Qy       1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500
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Db       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679


RESULT 10
US-09-978-564A-522
; Sequence 522, Application US/09978564A
; Publication No. US20030050241A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C25
;  CURRENT APPLICATION NUMBER: US/09/978,564A
;  CURRENT FILING DATE:  2001-10-16
;  PRIOR APPLICATION NUMBER: 09/918585
;  PRIOR FILING DATE: 2001-07-30
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;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1679; DB 11; Length 1679;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60

Qy         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120
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Db         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120

Qy        121 AAGAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180
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Db        121 AAGAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180

Qy        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240
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Db        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240

Qy        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300
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Qy        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
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Db        721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCCGTGGTACGGAGAGTAAA 780

Qy        781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840
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RESULT 9
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; Sequence 522, Application US/09978403A
; Publication No. US20030050240A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C17
;  CURRENT APPLICATION NUMBER: US/09/978,403A
;  CURRENT FILING DATE:  2002-03-19
;  PRIOR APPLICATION NUMBER: 09/918585
;  PRIOR FILING DATE: 2001-07-30
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR APPLICATION NUMBER: 60/085573
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1679; DB 11; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120
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Qy        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300
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; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C4
; CURRENT APPLICATION NUMBER: US/09/978,191A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
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; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081952
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082700
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
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; PRIOR APPLICATION NUMBER: 60/082796
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: 60/083336
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083392
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083554
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083558
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083500
; PRIOR FILING DATE: 1998-04-29

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;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C15
;  CURRENT APPLICATION NUMBER: US/09/978,585A
;  CURRENT FILING DATE:  2001-10-16
;  NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 522
;   LENGTH: 1679
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-978-585A-522

  Query Match           100.0%;  Score 1679;  DB 11;  Length 1679;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1679;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60
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Db          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60

Qy         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120
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Db         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120

Qy        121 AAGAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180
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Db        121 AAGAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180

Qy        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240
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Db        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240

Qy        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300
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Db        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300

Qy        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
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Db        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360

Qy        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420
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Db        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420

Qy        421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
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Db        421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480

Qy        481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540
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Db        481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540

Qy        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
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Db        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600

Qy        601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660
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Db        601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660

Qy        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720

Qy        721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAA 780

Qy        781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840

Qy        841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900

Qy        901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960

Qy        961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020

Qy       1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080
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Db       1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080

Qy       1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140

Qy       1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200

Qy       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260

Qy       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320

Qy       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380
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Db       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380

Qy       1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440

Qy       1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500
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Db       1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500

Qy       1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560
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Db       1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560

Qy       1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620

Qy       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
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Db       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679

RESULT 8
US-09-978-191A-522
; Sequence 522, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
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  Query Match           100.0%;  Score 1679;  DB 11;  Length 1679;
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  Matches 1679;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60

Qy         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120
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Db         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120

Qy        121 AAGAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180
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Qy        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240
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Db        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240

Qy        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300
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Db        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300

Qy        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
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Db        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360

Qy        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420
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Db        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420

Qy        421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
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Db        421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480

Qy        481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540
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Db        481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540

Qy        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
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Db        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600

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Db        601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660

Qy        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
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Db        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720

Qy        721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAA 780
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Db        721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAA 780

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Db        781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840

Qy        841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900
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Db        841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900

Qy        901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960
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Db        901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960

Qy        961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020
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Db       1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080

Qy       1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140
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Db       1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140

Qy       1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200
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Db       1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200

Qy       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
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Db       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260

Qy       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320
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Db       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320

Qy       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380
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Db       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380

Qy       1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440
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Db       1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440

Qy       1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500
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Db       1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500

Qy       1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560
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Db       1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560

Qy       1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620
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Db       1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620

Qy       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
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Db       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679

RESULT 7
US-09-978-585A-522
; Sequence 522, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
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Qy       181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240
Db       181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240

Qy       241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300
Db       241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300

Qy       301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
Db       301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360

Qy       361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420
Db       361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420

Qy       421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
Db       421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480

Qy       481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540
Db       481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540

Qy       541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
Db       541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600

Qy       601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660
Db       601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660

Qy       661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
Db       661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720

Qy       721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAA 780
Db       721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAA 780

Qy       781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840
Db       781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840

Qy       841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900
Db       841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900

Qy       901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960
Db       901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960

Qy       961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020
Db       961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020

Qy      1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080
Db      1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080

Qy      1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140
Db      1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140

Qy      1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200
Db      1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200

Qy      1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
Db      1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260

Qy      1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320
Db      1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320

Qy      1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380
Db      1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380

Qy      1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440
Db      1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440

Qy      1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500
Db      1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500

Qy      1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560
Db      1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560

Qy      1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620
Db      1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620

Qy      1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
Db      1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
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RESULT 6
US-09-978-608A-522
; Sequence 522, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C22
;  CURRENT APPLICATION NUMBER: US/09/978,608A
;  CURRENT FILING DATE:  2001-10-16
;  NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 522
;   LENGTH: 1679
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-978-608A-522
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Query Match 100.0%; Score 1679; DB 11; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60

Qy         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120
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Query Match 100.0%; Score 1806; DB 11; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.7e-150;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60

Qy         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120
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Qy        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180
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Qy        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240
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Qy        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300
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RESULT 9
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; Publication No. US20030050240A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C17
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; PRIOR APPLICATION NUMBER: 09/918585
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1806; DB 11; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.7e-150;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 10
US-09-978-564A-523
; Sequence 523, Application US/09978564A
; Publication No. US20030050241A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C25
; CURRENT APPLICATION NUMBER: US/09/978,564A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
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; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1806; DB 11; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.7e-150;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120
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RESULT 11
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; Sequence 523, Application US/09999833A
; Publication No. US20030054405A1
; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
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; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C65
; CURRENT APPLICATION NUMBER: US/09/999,833A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
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; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1806; DB 11; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.7e-150;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60
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Db          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60

Qy         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120
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Db         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120

Qy        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180
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Db        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180

Qy        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240
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Db        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240

Qy        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300
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Db        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300

Qy        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
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Db        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344


RESULT 12
US-09-981-915A-523
; Sequence 523, Application US/09981915A
; Publication No. US20030054986A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers; Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C12
;  CURRENT APPLICATION NUMBER: US/09/981,915A
;  CURRENT FILING DATE:  2001-10-16
;  PRIOR APPLICATION NUMBER: 09/918585
;  PRIOR FILING DATE: 2001-07-30
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/064249
;  PRIOR FILING DATE: 1997-11-03
;  PRIOR APPLICATION NUMBER: 60/065311
;  PRIOR FILING DATE: 1997-11-13
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;  PRIOR FILING DATE: 1997-11-21
;  PRIOR APPLICATION NUMBER: 60/077450
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;  PRIOR FILING DATE: 1998-04-23
;  PRIOR APPLICATION NUMBER: 60/083336
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; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1806; DB 11; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.7e-150;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60
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Db          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60

Qy         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120
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Db         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120

Qy        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180

Qy        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240
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Db        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240

Qy        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300
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Db        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300

Qy        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
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Db        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
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RESULT 13
US-09-978-824-523
; Sequence 523, Application US/09978824
; Publication No. US20030055216A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C14
; CURRENT APPLICATION NUMBER: US/09/978,824
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/085704
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/085697

  Query Match             100.0%;  Score 1806;  DB 11;  Length 344;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-150;
  Matches  344;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60
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Db          1 MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTID 60

Qy         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120
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Qy        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180
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Db        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180

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Qy        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
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RESULT 14
US-09-918-585A-523
; Sequence 523, Application US/09918585A
; Publication No. US20030060406A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C1
;  CURRENT APPLICATION NUMBER: US/09/918,585A
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/064249
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;  PRIOR APPLICATION NUMBER: 60/081955
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086023

Query Match 100.0%; Score 1806; DB 11; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.7e-150;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120
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Db         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120

Qy        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180
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Db        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180

Qy        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240
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Db        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240

Qy        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300
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RESULT 15
US-09-978-423A-523
; Sequence 523, Application US/09978423A
; Publication No. US20030069178A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
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; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C21
; CURRENT APPLICATION NUMBER: US/09/978,423A
; CURRENT FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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Query Match 100.0%; Score 1806; DB 11; Length 344;
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Qy         61 NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTD 120
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Qy        121 NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        181 SEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGT 240
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Qy        241 LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNK 300
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Qy        301 LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
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Job time : 53 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 11, 2003, 03:06:34 ; Search time 4576 Seconds
(without alignments)
3075.374 Million cell updates/sec

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Perfect score: 1806
Sequence: 1 MKTIQPKMHNSISWAIFTGL.....RRAGCVWLLPLLVLHLLLKF 344

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1806	100.0	1679	6	AX358872	AX358872 Sequence
2	1806	100.0	1679	6	AX362365	AX362365 Sequence
3	1806	100.0	1679	6	AX403748	AX403748 Sequence
4	1806	100.0	1679	6	AX454470	AX454470 Sequence
5	1806	100.0	1679	6	AX464242	AX464242 Sequence
6	1806	100.0	1679	6	AX490948	AX490948 Sequence
7	1665.5	92.2	1839	6	AX665342	AX665342 Sequence
8	1665.5	92.2	1839	9	AF126426	AF126426 Homo sapi
9	1650	91.4	1068	6	AX665344	AX665344 Sequence
10	1647.5	91.2	1615	10	BC023307	BC023307 Mus muscu
11	1644	91.0	1104	6	AX665346	AX665346 Sequence
12	1639.5	90.8	2040	10	RNU16845	U16845 Rattus norv
13	1638	90.7	1140	6	AX665348	AX665348 Sequence
14	1616.5	89.5	1410	10	AF282980	AF282980 Mus muscu
15	1500.5	83.1	1325	9	BC050716	BC050716 Homo sapi
16	1477.5	81.8	1257	5	GGCEPU1	Z72497 G.gallus mR
17	1428	79.1	1058	5	AF292935	AF292935 Gallus ga
18	1427.5	79.0	1035	5	AB011810	AB011810 Gallus ga
19	1393	77.1	1638	12	AF271233	AF271233 Synthetic
20	1357.5	75.2	1013	5	AF292936	AF292936 Gallus ga
21	1306.5	72.3	3216	5	GGCEPUS	AJ225897 Gallus ga
22	1306	72.3	1533	5	FFNINH55A	Y08170 Gallus gall
23	1286.5	71.2	3069	10	RATCALMA	M88709 Rattus norv
24	1275.5	70.6	1556	5	AF292934	AF292934 Gallus ga
25	1271.5	70.4	2935	12	AF271618	AF271618 Synthetic
26	1268	70.2	1478	9	HUMOBCAM	L34774 Human (clon
27	1268	70.2	3110	6	AX665340	AX665340 Sequence
28	1267	70.2	2593	4	BTOBCAM	X12672 Bovine mRNA
29	1259	69.7	2179	10	RATCALMB	M88710 Rattus norv
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31	951	52.7	756	12	AF271232	AF271232 Synthetic
32	946	52.4	1107	5	GGLAMPG9	Z94718 G.gallus mR
33	938.5	52.0	1158	5	GGLAMPG19	Z94720 G.gallus mR
34	938.5	52.0	2050	5	GGE19SPRO	Y08171 Gallus gall
35	932.5	51.6	1640	9	BC033803	BC033803 Homo sapi
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37	930.5	51.5	1194	5	GGLAMPG11	Z94719 G.gallus mR
38	926.5	51.3	1014	6	AR030577	AR030577 Sequence
39	926.5	51.3	1014	6	AR220260	AR220260 Sequence
40	926.5	51.3	1238	6	AR030575	AR030575 Sequence
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ALIGNMENTS

RESULT 1

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AX358872
LOCUS       AX358872               1679 bp    DNA     linear   PAT 13-FEB-2002
DEFINITION  Sequence 125 from Patent WO0193983.
ACCESSION   AX358872
VERSION     AX358872.1  GI:18675337
KEYWORDS
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,
            Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
            Watanabe,C.K. and Wood,W.I.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
  JOURNAL   Patent: WO 0193983-A 125 13-DEC-2001;
            Genentech Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1679
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT      498 a    432 c    419 g    330 t
ORIGIN

Alignment Scores:
Pred. No.:                6.67e-158      Length:          1679
Score:                    1806.00        Matches:         344
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       6              Gaps:            0

US-10-017-084A-523 (1-344) x AX358872 (1-1679)

Qy          1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
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Qy         21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
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Qy         41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
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Db        314 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 373

Qy         81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
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Db        374 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 433

Qy        101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
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Db        434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493

Qy        121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
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Qy        241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
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Qy        281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
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Qy        321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
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Qy        341 LeuLeuLysPhe 344
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RESULT 2
AX362365
LOCUS       AX362365               1679 bp    DNA     linear   PAT 15-FEB-2002
DEFINITION  Sequence 125 from Patent WO0208288.
ACCESSION   AX362365
VERSION     AX362365.1  GI:18694640
KEYWORDS
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,
            Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
            Watanabe,C.K. and Wood,W.I.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
  JOURNAL   Patent: WO 0208288-A 125 31-JAN-2002;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1679
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT      498 a    432 c    419 g    330 t
ORIGIN

Alignment Scores:
Pred. No.:                6.67e-158      Length:          1679
Score:                    1806.00        Matches:         344
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       6              Gaps:            0

US-10-017-084A-523 (1-344) x AX362365 (1-1679)

Qy          1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
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Qy           21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
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Db          194 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 253

Qy           41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
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Qy           61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
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Qy          181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
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Db          674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy          201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
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Db          734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy          221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
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Db          794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853

Qy          241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
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Db          974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

Qy          301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
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Db         1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1093

Qy          321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
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Db         1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1153

Qy          341 LeuLeuLysPhe 344
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RESULT 3
AX403748

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LOCUS       AX403748                1679 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 103 from Patent WO0077037.
ACCESSION   AX403748
VERSION     AX403748.1  GI:21437184
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ashkenazi,A., Baker,K., Botstein,D., Desnoyers,L., Eaton,D.L.,
            Ferrara,N., Fong,S., Gao,W.Q., Gerber,H., Gerritsen,M.E.,
            Goddard,A., Godowski,P., Gurney,A., Kljavin,I.J., Mather,J.,
            Napier,M., Pan,J., Paoni,N., Roy,M., Tumas,D., Watanabe,C.,
            Williams,P.M., Wood,W.I. and Zhang,Z.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
  JOURNAL   Patent: WO 0077037-A 103 21-DEC-2000;
            Genentech Inc. (US)
FEATURES             Location/Qualifiers
     source          1..1679
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT      498 a    432 c    419 g    330 t
ORIGIN

Alignment Scores:
Pred. No.:               6.67e-158     Length:          1679
Score:                   1806.00       Matches:         344
Percent Similarity:      100.00%       Conservative:    0
Best Local Similarity:   100.00%       Mismatches:      0
Query Match:             100.00%       Indels:          0
DB:                      6             Gaps:            0

US-10-017-084A-523 (1-344) x AX403748 (1-1679)

Qy            1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
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Qy           41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
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Qy           81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
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Qy          141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
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Db          554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613

Qy          161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
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Db          614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673
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Qy        181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
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Db        674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy        201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
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Db        734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy        221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
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Db        794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853

Qy        241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
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Db        854 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 913

Qy        261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
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Db        914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 973

Qy        281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
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Db        974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

Qy        301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
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Db       1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1093

Qy        321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
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Db       1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1153

Qy        341 LeuLeuLysPhe 344
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Db       1154 CTTCTCAAATTT 1165

RESULT 4
AX454470
LOCUS       AX454470               1679 bp    DNA     linear   PAT 06-JUL-2002
DEFINITION  Sequence 55 from Patent WO0208284.
ACCESSION   AX454470
VERSION     AX454470.1  GI:21713859
KEYWORDS
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
            Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
            Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
            and Ye,W.
  TITLE     Compositions and methods for the diagnosis and treatment of
            disorders involving angiogenesis
  JOURNAL   Patent: WO 0208284-A 55 31-JAN-2002;
            Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
            (US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,
            Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
            Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)
            ; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;
            Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
            I. (US)
FEATURES             Location/Qualifiers
     source          1. .1679
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT      498 a    432 c    419 g    330 t
ORIGIN

Alignment Scores:
Pred. No.:              6.67e-158       Length:         1679
Score:                  1806.00         Matches:        344
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Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-10-017-084A-523 (1-344) x AX454470 (1-1679)

Qy          1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
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Db        134 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 193

Qy         21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
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Db        194 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 253

Qy         41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
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Db        254 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 313

Qy         61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
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Db        314 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 373

Qy         81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
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Db        374 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 433

Qy        101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
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Db        434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493

Qy        121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
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Qy        141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
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Qy        161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
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Db        614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673

Qy        181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
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Db        674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy        201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
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Db        734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy        221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853

Qy        241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        854 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 913

Qy        261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
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Db        914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 973

Qy        281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

Qy        301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
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Db       1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1093

Qy        321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
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Db       1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1153

Qy        341 LeuLeuLysPhe 344
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Db       1154 CTTCTCAAATTT 1165

RESULT 5
AX464242
LOCUS       AX464242               1679 bp    DNA     linear   PAT 16-JUL-2002
DEFINITION  Sequence 375 from Patent WO0140466.
ACCESSION   AX464242
VERSION     AX464242.1  GI:21899137
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Beresini,M., Deforge,L., Desnoyers,L., Filvaroff,E.,
            Gao,W.Q., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L.,
            Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K.,
            Wood,W.L. and Zhang,Z.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            same
  JOURNAL   Patent: WO 0140466-A 375 07-JUN-2001;
            Genentech Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1679
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT      498 a    432 c    419 g    330 t
ORIGIN

Alignment Scores:
Pred. No.:              6.67e-158      Length:         1679
Score:                  1806.00        Matches:        344
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     6              Gaps:           0

US-10-017-084A-523 (1-344) x AX464242 (1-1679)

Qy          1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
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Db        134 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 193

Qy         21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
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Db        194 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 253

Qy         41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
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Db        254 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 313

Qy         61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
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Db        314 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 373

Qy         81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
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Db        374 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 433

Qy        101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
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Db        434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493

Qy        121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
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Db        494 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 553

Qy        141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
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Qy        161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
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Db        614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673

Qy        181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
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Db        674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy        201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
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Db        734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy        221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853

Qy        241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
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Db        854 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 913

Qy        261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
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Db        914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 973

Qy        281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
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Db        974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

Qy        301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
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Db       1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1153

Qy        341 LeuLeuLysPhe 344
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Db       1154 CTTCTCAAATTT 1165

RESULT 6
AX490948
LOCUS       AX490948               1679 bp    DNA     linear   PAT 16-AUG-2002
DEFINITION  Sequence 55 from Patent WO0200690.
ACCESSION   AX490948
VERSION     AX490948.1  GI:22323811
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
            Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
            Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
            and Ye,W.
  TITLE     Compositions and methods for the diagnosis and treatment of
            disorders involving angiogenesis
  JOURNAL   Patent: WO 0200690-A 55 03-JAN-2002;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1679
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT      498 a    432 c    419 g    330 t
ORIGIN

Alignment Scores:
Pred. No.:              6.67e-158      Length:         1679
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Score:                 1806.00       Matches:       344
Percent Similarity:    100.00%       Conservative:  0
Best Local Similarity: 100.00%       Mismatches:    0
Query Match:           100.00%       Indels:        0
DB:                    6             Gaps:          0

US-10-017-084A-523 (1-344) x AX490948 (1-1679)

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Qy         21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
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Qy         41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
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Db        254 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 313

Qy         61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
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Db        314 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 373

Qy         81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
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Db        374 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 433

Qy        101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
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Qy        121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
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Db        494 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 553

Qy        141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
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Qy        161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
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Db        614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673

Qy        181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy        201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
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Db        734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy        221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
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Db        794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853

Qy        241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
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Db        854 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 913

Qy        261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 973

Qy        281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

Qy        301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1093

Qy        321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1153

Qy        341 LeuLeuLysPhe 344
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Db       1154 CTTCTCAAATTT 1165
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RESULT 7
AX665342
LOCUS       AX665342               1839 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 100 from Patent WO03002765.
ACCESSION   AX665342
VERSION     AX665342.1  GI:29290464
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Sellar,G.C. and Gabra,H.
  TITLE     Cancer
  JOURNAL   Patent: WO 03002765-A 100 09-JAN-2003;
            Cancer Research Technology Limited (GB)
FEATURES             Location/Qualifiers
     source          1..1839
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT      464 a    506 c    503 g    366 t
ORIGIN

Alignment Scores:
Pred. No.:             8.13e-145     Length:        1839
Score:                 1665.50       Matches:       322
Percent Similarity:    97.31%        Conservative:  3
Best Local Similarity: 96.41%        Mismatches:    8
Query Match:           92.22%        Indels:        2
DB:                    6             Gaps:          1

US-10-017-084A-523 (1-344) x AX665342 (1-1839)

Qy         11 SerIleSerTrpAlaIlePheThrGlyLeuAlaAlaLeuCysLeuPheGlnGlyValPro 30
              |||   |||||:::      :::|||      :::|||           |||||||||
Db        299 AGTGCCTCGTGGTCGTGTCTCTCAGGCTGCTGTTCCTTG---TACCC-ACAGGAGTGCCC 354

Qy         31 ValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArgGlnGly 50
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 GTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGG 414

Qy         51 GluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsn 70
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 GAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAAC 474

Qy         71 ArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeu 90
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 CGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTT 534

Qy         91 LeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyrAspGlu 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 CTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAG 594

Qy        111 GlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeu 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 GGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTC 654

Qy        131 IleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGly 150
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 ATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGG 714

Qy        151 AsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArg 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 AACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGA 774
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Qy       171 HisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGly 190
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Db       775 CACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGC 834

Qy       191 IleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaPro 210
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Db       835 ATCACCCGGGAACAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCC 894

Qy       211 ValValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGly 230
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Db       895 GTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGT 954

Qy       231 ThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSer 250
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Db       955 ACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCA 1014

Qy       251 AlaGluPheGlnTrpTyrLysAspAspLysArgLeuIleGluGlyLysLysGlyValLys 270
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Db      1015 GCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAA 1074

Qy       271 ValGluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyr 290
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Db      1075 GTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTAT 1134

Qy       291 GlyAsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeu 310
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Db      1135 GGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTA 1194

Qy       311 PheGlyProGlyAlaValSerGluValSerAsnGlyThrSerArgArgAlaGlyCysVal 330
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1195 TTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTC 1254

Qy       331 TrpLeuLeuProLeuLeuValLeuHisLeuLeuLeuLysPhe 344
             ||||||||||||||||||||||||||||||||||||||||||
Db      1255 TGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTT 1296
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RESULT 8
AF126426
LOCUS       AF126426                1839 bp    mRNA    linear   PRI 10-JUN-2002
DEFINITION  Homo sapiens neurotrimin (HNT) mRNA, complete cds.
ACCESSION   AF126426
VERSION     AF126426.1  GI:7158997
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1839)
  AUTHORS   Li,G., Jin,J., Tan,X., Hu,S., Yuan,J. and Qiang,B.
  TITLE     Cloning and identification of human neurotrimin full length cDNA
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1839)
  AUTHORS   Li,G., Jin,J., Tan,X., Hu,S., Yuan,J. and Qiang,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-FEB-1999) Biochemistry, Institute of Basic Medical
            Sciences, 5 Dong Dan San Tiao, Beijing 100005, PR China
FEATURES             Location/Qualifiers
     source          1..1839
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
     gene            1..1839
                     /gene="HNT"
     CDS             265..1299
                     /gene="HNT"
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                     /codon_start=1
                     /product="neurotrimin"
                     /protein_id="AAF37591.1"
                     /db_xref="GI:7158998"
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                     QNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIAT
                     GRPEPTVTWRHISPKAVGFVSEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVT
                     VNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPF
                     LSKLIFFNVSEHDYGNYTCVASNKLGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLP
                     LLVLHLLLKF"
BASE COUNT      464 a    506 c    503 g    366 t
ORIGIN

Alignment Scores:
Pred. No.:             8.13e-145      Length:          1839
Score:                 1665.50        Matches:         322
Percent Similarity:    97.31%         Conservative:    3
Best Local Similarity: 96.41%         Mismatches:      8
Query Match:           92.22%         Indels:          2
DB:                    9              Gaps:            1

US-10-017-084A-523 (1-344) x AF126426 (1-1839)

Qy        11 SerIleSerTrpAlaIlePheThrGlyLeuAlaAlaLeuCysLeuPheGlnGlyValPro 30
             |||  ||||||:::    :::|||      :::|||        |||||||||
Db       299 AGTGCCTCGTGGTCGTGTCTCTCAGGCTGCTGTTCCTTG---TACCC-ACAGGAGTGCCC 354

Qy        31 ValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArgGlnGly 50
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       355 GTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGG 414

Qy        51 GluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsn 70
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       415 GAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAAC 474

Qy        71 ArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeu 90
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       475 CGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTT 534

Qy        91 LeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyrAspGlu 110
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       535 CTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAG 594

Qy       111 GlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeu 130
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       595 GGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTC 654

Qy       131 IleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGly 150
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       655 ATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGG 714

Qy       151 AsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArg 170
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Db       715 AACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGA 774

Qy       171 HisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGly 190
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Db       775 CACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGC 834

Qy       191 IleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaPro 210
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Db       835 ATCACCCGGGAACAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCC 894

Qy       211 ValValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGly 230
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       895 GTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGT 954

Qy       231 ThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSer 250
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       955 ACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCA 1014

Qy       251 AlaGluPheGlnTrpTyrLysAspAspLysArgLeuIleGluGlyLysLysGlyValLys 270
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1015 GCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAA 1074

Qy       271 ValGluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyr 290
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1075 GTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTAT 1134
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Qy        291 GlyAsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeu 310
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Db       1135 GGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTA 1194

Qy        311 PheGlyProGlyAlaValSerGluValSerAsnGlyThrSerArgArgAlaGlyCysVal 330
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1195 TTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTC 1254

Qy        331 TrpLeuLeuProLeuLeuValLeuHisLeuLeuLeuLysPhe 344
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Db       1255 TGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTT 1296

RESULT 9
AX665344
LOCUS       AX665344               1068 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 102 from Patent WO03002765.
ACCESSION   AX665344
VERSION     AX665344.1  GI:29290465
KEYWORDS
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Sellar,G.C. and Gabra,H.
  TITLE     Cancer
  JOURNAL   Patent: WO 03002765-A 102 09-JAN-2003;
            Cancer Research Technology Limited (GB)
FEATURES             Location/Qualifiers
     source          1..1068
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT      268 a    290 c    287 g    223 t
ORIGIN

Alignment Scores:
Pred. No.:              1.12e-143       Length:         1068
Score:                  1650.00         Matches:        322
Percent Similarity:     94.20%          Conservative:   3
Best Local Similarity:  93.33%          Mismatches:     8
Query Match:            91.36%          Indels:         13
DB:                     6               Gaps:           2

US-10-017-084A-523 (1-344) x AX665344 (1-1068)

Qy         11 SerIleSerTrpAlaIlePheThrGlyLeuAlaAlaLeuCysLeuPheGlnGlyValPro 30
              |||   ||||||:::      :::|||     :::|||           |||||||||
Db         35 AGTGCCTCGTGGTCGTGTCTCTCAGGCTGCTGTTCCTTG---TACCC-ACAGGAGTGCCC 90

Qy         31 ValArgSerGlyAspAlaThrProProLysAlaMetAspAsnValThrValArgGlnGly 50
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Db         91 GTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGG 150

Qy         51 GluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsn 70
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAAC 210

Qy         71 ArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeu 90
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 CGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTT 270

Qy         91 LeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyrAspGlu 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 CTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAG 330

Qy        111 GlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeu 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 GGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTC 390

Qy        131 IleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGly 150
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Db        391 ATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGG 450

Qy        151 AsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArg 170
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Qy        171 HisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGly 190
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Qy        191 IleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaPro 210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 ATCACCCGGGAACAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCC 630

Qy        211 ValValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGly 230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        631 GTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGT 690

Qy        231 ThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSer 250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        691 ACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCA 750

Qy        251 AlaGluPheGlnTrpTyrLysAspAspLysArgLeuIleGluGlyLysLysGlyValLys 270
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Db        751 GCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAA 810

Qy        271 ValGluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyr 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        811 GTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTAT 870

Qy        291 GlyAsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeu 310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        871 GGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTA 930

Qy        311 Phe--------------------------------GlyProGlyAlaValSerGluVal 319
              |||                               ||||||||||||||||||||||
Db        931 TTTGAAGTGAAAACTACAGCCCTGACCCCTTGGAAAGGTCCAGGCGCCGTCAGCGAGGTG 990

Qy        320 SerAsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHis 339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        991 AGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCAC 1050

Qy        340 LeuLeuLeuLysPhe 344
              |||||||||||||||
Db       1051 CTGCTTCTCAAATTT 1065

RESULT 10
BC023307
LOCUS       BC023307               1615 bp    mRNA    linear   ROD 10-JUN-2003
DEFINITION  Mus musculus neurotrimin, mRNA (cDNA clone MGC:30504
            IMAGE:4480983), complete cds.
ACCESSION   BC023307
VERSION     BC023307.1  GI:23958300
KEYWORDS    MGC.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1615)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
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            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
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            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1615)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-FEB-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: The Cepko Laboratory
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: amg@bcm.tmc.edu
            Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
            Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
            A.N., Gibbs, R.A.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 41 Row: h Column: 10
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 26986610.
FEATURES             Location/Qualifiers
     source          1..1615
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                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="MGC:30504 IMAGE:4480983"
                     /tissue_type="Eye, retina, mouse strain C57Bl\6"
                     /clone_lib="NIH_MGC_94"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
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                     /gene="Hnt-pending"
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                     /db_xref="MGI:2446259"
     CDS             44..1078
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                     /product="neurotrimin"
                     /protein_id="AAH23307.1"
                     /db_xref="GI:23958301"
                     /db_xref="LocusID:235106"
                     /translation="MGVCGYLFLPWKCLVVVSLRLLFLVPTGVPVRSGDATFPKAMDN
                     VTVRQGESATLRCTIDNRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEI
                     QNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIAT
                     GRPEPTVTWRHISPKAVGFVSEDEYLEIQGITREQSGEYECSASNDVAAPVVRRVKVT
                     VNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWFKDDKRLVEGKKGVKVENRPF
                     LSKLTFFNVSEHDYGNYTCVASNKLGHTNASIMLFGPGAVSEVNNGTSRRAGCIWLLP
                     LLVLHLLLKF"
BASE COUNT      442 a    403 c    428 g    342 t
ORIGIN

Alignment Scores:
Pred. No.:              3.23e-143      Length:         1615
Score:                  1647.50        Matches:        314
Percent Similarity:     95.83%         Conservative:   8
Best Local Similarity:  93.45%         Mismatches:     11
Query Match:            91.22%         Indels:         3
DB:                     10             Gaps:           1

US-10-017-084A-523 (1-344) x BC023307 (1-1615)

Qy         12 IleSerTrpAlaIlePheThrGlyLeuAlaAlaLeuCysLeuPhe---------GlnGly 28
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Db         68 CTGCCCTGGAAGTGCCTCGTGGTCGTGTCTCTCAGGCTGCTATTCCTTGTACCCACAGGA 127

Qy         29 ValProValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArg 48
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 GTGCCGGTGCGTAGCGGAGATGCCACCTTTCCCAAAGCTATGGACAACGTGACGGTCAGG 187

Qy         49 GlnGlyGluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrp 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 CAGGGGGAGAGCGCCACCCTCAGGTGCACAATTGACAACCGAGTCACCCGGGTGGCCTGG 247

Qy         69 LeuAsnArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgVal 88
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 CTAAACCGCAGTACCATCCTCTATGCTGGAAATGACAAGTGGTGCCTAGATCCTCGTGTG 307

Qy         89 ValLeuLeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyr 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 GTCCTCCTGAGTAACACCCAGACCCAGTACAGCATTGAGATCCAGAATGTGGATGTGTAC 367

Qy        109 AspGluGlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgVal 128
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Db        368 GATGAGGGCCCTTATACCTGCTCGGTACAGACAGACAACCACCCTAAGACCTCCAGGGTC 427

Qy        129 HisLeuIleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsn 148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        428 CACCTCATTGTACAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAAT 487

Qy        149 GluGlyAsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThr 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        488 GAAGGGAACAACATCAGCCTCACTTGCATAGCCACAGGTAGACCGGAGCCTACAGTAACC 547

Qy        169 TrpArgHisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIle 188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        548 TGGAGACATATTTCTCCCAAGGCCGTTGGCTTTGTGAGTGAGGATGAGTACCTGGAGATC 607

Qy        189 GlnGlyIleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAla 208
              |||||||||||||||||||||||||||:::||||||||||||||||||||||||||||||
Db        608 CAGGGCATCACTCGGGAACAGTCAGGCGAGTACGAGTGCAGCGCCTCCAACGACGTGGCG 667

Qy        209 AlaProValValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAla 228
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Db        668 GCACCAGTGGTACGAAGAGTGAAGGTCACCGTGAACTATCCACCATACATCTCAGAAGCT 727

Qy        229 LysGlyThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaVal 248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        728 AAGGGCACAGGTGTCCCCGTGGGGCAGAAGGGGACTCTGCAGTGTGAAGCTTCCGCAGTC 787

Qy        249 ProSerAlaGluPheGlnTrpTyrLysAspAspLysArgLeuIleGluGlyLysLysGly 268
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Db        788 CCTTCAGCAGAATTTCAATGGTTCAAGGATGACAAAAGACTGGTCGAAGGAAAGAAGGGA 847

Qy        269 ValLysValGluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHis 288
              ||||||||||||||||||||||||||||||||||||   |||||||||||||||||||||
Db        848 GTCAAAGTGGAAAACAGACCTTTCCTTTCAAAACTCACCTTTTTCAACGTCTCTGAACAT 907

Qy        289 AspTyrGlyAsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIle 308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        908 GACTATGGGAACTACACATGTGTGGCCTCCAACAAGCTGGGTCACACCAACGCCAGCATC 967

Qy        309 MetLeuPheGlyProGlyAlaValSerGluValSerAsnGlyThrSerArgArgAlaGly 328
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Db        968 ATGCTATTTGGTCCCGGTGCTGTCAGTGAGGTCAACAATGGGACATCAAGGAGGGCAGGC 1027

Qy        329 CysValTrpLeuLeuProLeuLeuValLeuHisLeuLeuLeuLysPhe 344
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RESULT 11
AX665346
LOCUS       AX665346                1104 bp    DNA     linear   PAT 26-MAR-2003
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DEFINITION  Sequence 104 from Patent WO03002765.
ACCESSION   AX665346
VERSION     AX665346.1  GI:29290466
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Sellar,G.C. and Gabra,H.
  TITLE     Cancer
  JOURNAL   Patent: WO 03002765-A 104 09-JAN-2003;
            Cancer Research Technology Limited (GB)
FEATURES             Location/Qualifiers
     source          1..1104
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
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BASE COUNT      280 a    298 c    294 g    232 t
ORIGIN

Alignment Scores:
Pred. No.:              4.2e-143        Length:         1104
Score:                  1644.00         Matches:        322
Percent Similarity:     91.04%          Conservative:   3
Best Local Similarity:  90.20%          Mismatches:     8
Query Match:            91.03%          Indels:         25
DB:                     6               Gaps:           2

US-10-017-084A-523 (1-344) x AX665346 (1-1104)

Qy         11 SerIleSerTrpAlaIlePheThrGlyLeuAlaAlaLeuCysLeuPheGlnGlyValPro 30
              |||   |||||:::      :::|||     :::|||              |||||||||
Db         35 AGTGCCTCGTGGTCGTGTCTCTCAGGCTGCTGTTCCTTG---TACCC-ACAGGAGTGCCC 90

Qy         31 ValArgSerGlyAspAlaThrProProLysAlaMetAspAsnValThrValArgGlnGly 50
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Db         91 GTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGG 150

Qy         51 GluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsn 70
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Db        151 GAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAAC 210

Qy         71 ArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeu 90
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Db        211 CGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTT 270

Qy         91 LeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyrAspGlu 110
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Db        271 CTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAG 330

Qy        111 GlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeu 130
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Db        331 GGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTC 390

Qy        131 IleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGly 150
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Db        391 ATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGG 450

Qy        151 AsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArg 170
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Db        451 AACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGA 510

Qy        171 HisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGly 190
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Db        511 CACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGC 570

Qy        191 IleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaPro 210
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Db        571 ATCACCCGGGAACAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCC 630

Qy        211 ValValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGly 230
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Db        631 GTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGT 690

Qy        231 ThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSer 250
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Db        691 ACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCA 750

Qy        251 AlaGluPheGlnTrpTyrLysAspAspLysArgLeuIleGluGlyLysLysGlyValLys 270
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Db        751 GCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAA 810

Qy        271 ValGluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyr 290
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Db        811 GTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTAT 870

Qy        291 GlyAsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeu 310
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Db        871 GGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTA 930

Qy        311 Phe------------------------------------------------------------ 311
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Db        931 TTTGAACTAAATGAGCCTACGAGCTCAACTTTGTTGCAAGAAGTGAAAACTACAGCCCTG 990

Qy        312 ------------GlyProGlyAlaValSerGluValSerAsnGlyThrSerArgArgAla 327
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Db        991 ACCCCTTGGAAAGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCA 1050

Qy        328 GlyCysValTrpLeuLeuProLeuLeuValLeuHisLeuLeuLeuLysPhe 344
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RESULT 12
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LOCUS       RNU16845                2040 bp    mRNA    linear   ROD 26-MAY-1995
DEFINITION  Rattus norvegicus neurotrimin mRNA, complete cds.
ACCESSION   U16845
VERSION     U16845.1  GI:755184
KEYWORDS    .
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 2040)
  AUTHORS   Struyk,A.F., Canoll,P.D., Wolfgang,M.J., Rosen,C.L., D'Eustachio,P.
            and Salzer,J.L.
  TITLE     Cloning of neurotrimin defines a new subfamily of differentially
            expressed neural cell adhesion molecules
  JOURNAL   J. Neurosci. 15 (3 Pt 2), 2141-2156 (1995)
  MEDLINE   95198094
   PUBMED   7891157
REFERENCE   2  (bases 1 to 2040)
  AUTHORS   Salzer,J.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-NOV-1994) James L. Salzer, Cell Biology, NYU Medical
            Center, 550 First Avenue, New York, NY 10016, USA
FEATURES             Location/Qualifiers
     source          1..2040
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                     /db_xref="GI:755185"
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                     GRPEPTVTWRHISPKAVGFVSEDEYLEIQGITREQSGEYECSASNDVAAPVVRRVNVT
                     VNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWFKDDKRLVEGKKGVKVENRPF
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BASE COUNT      504 a    544 c    551 g    441 t
ORIGIN

Alignment Scores:
Pred. No.:                2.4e-142        Length:          2040
Score:                    1639.50         Matches:         314
Percent Similarity:       96.71%          Conservative:    9
Best Local Similarity:    94.01%          Mismatches:      10
Query Match:              90.78%          Indels:          2
DB:                       10              Gaps:            1

US-10-017-084A-523 (1-344) x RNU16845 (1-2040)

Qy          11 SerIleSerTrpAlaIlePheThrGlyLeuAlaAlaLeuCysLeuPheGlnGlyValPro 30
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Db         518 AGTGCCTCGTGGTCGTGTCTCTCAGGCTGCTGTTCCTTG---TACCC-ACAGGAGTGCCG 573

Qy          31 ValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArgGlnGly 50
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Db         574 GTGCGTAGCGGAGATGCCACCTTTCCCAAAGCTATGGACAACGTGACGGTCAGGCAGGGG 633

Qy          51 GluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsn 70
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Db         634 GAGAGCGCCACCCTCAGGTGCACAATTGACAACCGAGTCACCCGGGTGGCCTGGCTAAAC 693

Qy          71 ArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeu 90
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Db         694 CGCAGTACCATCCTCTATGCTGGAAATGACAAGTGGTGCCTAGATCCTCGTGTGGTTCTC 753

Qy          91 LeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyrAspGlu 110
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Db         754 CTGAGTAACACCCAGACCCAGTACAGCATTGAGATCCAGAATGTGGATGTGTATGATGAG 813

Qy         111 GlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeu 130
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Db         814 GGCCCTTATACCTGCTCGGTGCAGACAGACAACCACCCTAAGACCTCCAGGGTCCACCTC 873

Qy         131 IleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGly 150
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Db         874 ATTGTACAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGG 933

Qy         151 AsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArg 170
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Db         934 AACAACATCAGCCTCACTTGCATAGCCACAGGTAGACCGGAGCCTACAGTAACCTGGAGA 993

Qy         171 HisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGly 190
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Db         994 CATATTTCTCCCAAAGCTGTCGGCTTTGTGAGTGAGGATGAGTACCTGGAGATCCAGGGC 1053

Qy         191 IleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaPro 210
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Db        1054 ATCACTCGGGAGCAGTCAGGCGAGTATGAGTGCAGCGCCTCCAACGACGTGGCAGCACCA 1113

Qy         211 ValValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGly 230
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Db        1114 GTCGTACGAAGAGTGAACGTCACCGTGAACTATCCACCATACATCTCAGAAGCTAAGGGT 1173

Qy         231 ThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSer 250
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Db        1174 ACAGGTGTCCCCGTGGGGCAGAAGGGGACTCTGCAGTGTGAAGCCTCGGCAGTCCCTTCA 1233

Qy         251 AlaGluPheGlnTrpTyrLysAspAspLysArgLeuIleGluGlyLysLysGlyValLys 270
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Db        1234 GCAGAATTTCAGTGGTTCAAGGATGACAAAAGACTGGTTGAAGGGAAGAAGGGAGTCAAA 1293

Qy         271 ValGluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyr 290
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Db        1294 GTGGAAAACAGACCTTTCCTTTCAAGACTCACCTTTTTCAACGTCTCTGAACACGACTAT 1353

Qy         291 GlyAsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeu 310
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Db        1354 GGGAACTACACATGTGTGGCATCCAACAAGTTGGGCCACACCAATGCCAGCATCATGCTA 1413

Qy         311 PheGlyProGlyAlaValSerGluValSerAsnGlyThrSerArgArgAlaGlyCysVal 330
               |||||||||||||||||||||||||:::||||||||||||||||||||||||||||:::
Db        1414 TTTGGCCCAGGTGCTGTCAGCGAGGTCAACAATGGGACGTCAAGGAGGGCAGGCTGCATT 1473

Qy         331 TrpLeuLeuProLeuLeuValLeuHisLeuLeuLeuLysPhe 344
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Db        1474 TGGCTCCTCCCTCTTCTGGTCTTACACCTGCTCCTCAAATTT 1515

RESULT 13
AX665348
LOCUS       AX665348                1140 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 106 from Patent WO03002765.
ACCESSION   AX665348
VERSION     AX665348.1  GI:29290467
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Sellar,G.C. and Gabra,H.
  TITLE     Cancer
  JOURNAL   Patent: WO 03002765-A 106 09-JAN-2003;
            Cancer Research Technology Limited (GB)
FEATURES             Location/Qualifiers
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BASE COUNT      289 a    304 c    304 g    243 t
ORIGIN

Alignment Scores:
Pred. No.:                1.58e-142       Length:          1140
Score:                    1638.00         Matches:         322
Percent Similarity:       88.08%          Conservative:    3
Best Local Similarity:    87.26%          Mismatches:      8
Query Match:              90.70%          Indels:          37
DB:                       6               Gaps:            2

US-10-017-084A-523 (1-344) x AX665348 (1-1140)

Qy          11 SerIleSerTrpAlaIlePheThrGlyLeuAlaAlaLeuCysLeuPheGlnGlyValPro 30
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Db          35 AGTGCCTCGTGGTCGTGTCTCTCAGGCTGCTGTTCCTTG---TACCC-ACAGGAGTGCCC 90

Qy          31 ValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArgGlnGly 50
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Db          91 GTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGG 150

Qy          51 GluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsn 70
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Db         151 GAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAAC 210

Qy          71 ArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeu 90
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         211 CGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTT 270

Qy          91 LeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyrAspGlu 110
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         271 CTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAG 330

Qy         111 GlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeu 130
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         331 GGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTC 390

Qy         131 IleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGly 150
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Db         391 ATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGG 450

Qy         151 AsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArg 170
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Db        451 AACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGA 510

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Db        511 CACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGC 570

Qy        191 IleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaPro 210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 ATCACCCGGGAACAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCC 630

Qy        211 ValValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGly 230
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Db        631 GTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGT 690

Qy        231 ThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSer 250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        691 ACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCA 750

Qy        251 AlaGluPheGlnTrpTyrLysAspAspLysArgLeuIleGluGlyLysLysGlyValLys 270
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        751 GCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAA 810

Qy        271 ValGluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyr 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        811 GTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTAT 870

Qy        291 GlyAsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeu 310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        871 GGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTA 930

Qy        311 Phe--------------------------------------------------------- 311
              |||
Db        931 TTTGATGGCTCCTAAGCTGACTGTGGGAATCATAATTGGAACTAAATGAGCCTACGAGC 990

Qy        312 ------------------------------------------------GlyProGlyAla 315
                                                              ||||||||||||
Db        991 TCAACTTTGTTGCAAGAAGTGAAAACTACAGCCCTGACCCCTTGGAAAGGTCCAGGCGCC 1050

Qy        316 ValSerGluValSerAsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeu 335
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1051 GTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTT 1110

Qy        336 LeuValLeuHisLeuLeuLeuLysPhe 344
              |||||||||||||||||||||||||||
Db       1111 CTGGTCTTGCACCTGCTTCTCAAATTT 1137
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RESULT 14
AF282980
LOCUS       AF282980                1410 bp    mRNA    linear   ROD 01-FEB-2001
DEFINITION  Mus musculus neurotrimin mRNA, complete cds.
ACCESSION   AF282980
VERSION     AF282980.1  GI:12642539
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1410)
  AUTHORS   Kim,T.H., Choi,S.C., Kim,J., Jeon,J.W., Kim,K.D. and Lee,S.H.
  TITLE     Cloning and expression of mouse neurotrimin gene in the developing
            nervous system
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1410)
  AUTHORS   Kim,T.H., Choi,S.C., Kim,J., Jeon,J.W., Kim,K.D. and Lee,S.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-JUN-2000) Graduate School of Biotechnology, Korea
            University, 1,5-ka Anam-dong Sungbuk-ku, Seoul 136-701, Korea
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:10090"
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                     /product="neurotrimin"
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                     QNVDVYDEGPYTCSVQIDNHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIAT
                     GRPEPTVTWRHISPKAVGFVSEDEYLQIQGITREQSGEYECSASNDVAAPVVPRVKVT
                     VNYPPYFSEAKGTGVPVGQKGTLQCEASAVPSAEFQWFKDDKRLVEGKKGVKVENRPF
                     LSKLTFFNVSEHDYGNYTCVASNKLGHTNASIMLFGPGAVSEVNNGTSRRAGCIWLLP
                     LLVLHLLLKF"
BASE COUNT      369 a    365 c    368 g    308 t
ORIGIN

Alignment Scores:
Pred. No.:              2.04e-140      Length:         1410
Score:                  1616.50        Matches:        308
Percent Similarity:     94.35%         Conservative:   9
Best Local Similarity:  91.67%         Mismatches:     16
Query Match:            89.51%         Indels:         3
DB:                     10             Gaps:           1

US-10-017-084A-523 (1-344) x AF282980 (1-1410)
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Qy         12 IleSerTrpAlaIlePheThrGlyLeuAlaAlaLeuCysLeuPhe---------GlnGly 28
              :::   |||            ::::::          ||||||          |||
Db         25 CTGCCCTGGAAGTGCCTCGTGGTCGTGTCTCTCAGGCTGCTATTCCTTGTACCCACAGGA 84

Qy         29 ValProValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArg 48
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 GTGCCGGTGCGTAGCGGAGATGCTACCTTTCCCAAAGCTATGGACAACGTGACGGTCAGG 144

Qy         49 GlnGlyGluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrp 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 CAGGGGGAGAGCGCCACCCTCAGGTGCACAATTGACAACCGAGTCACCCGGGTGGCCTGG 204

Qy         69 LeuAsnArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgVal 88
              |||||||||||||||||| . |||||||||||||||||||||||||||||||||||||||
Db        205 CTAAACCGCAGTACCATCCCCTATGCTGGAAATGACAAGTGGTGCCTAGATCCTCGTGTG 264

Qy         89 ValLeuLeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyr 108
              |||||||||  |||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 GTCCTCCTGGGTAACACCCAGACCCAGTACAGCATTGAGATCCAGAATGTGGATGTGTAC 324

Qy        109 AspGluGlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgVal 128
              ||||||||||||||||||||||||||||||    ||||||||||||||||||||||||||
Db        325 GATGAGGGCCCTTATACCTGCTCGGTACAGATAGACAATCACCCTAAGACCTCCAGGGTC 384

Qy        129 HisLeuIleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsn 148
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Qy        149 GluGlyAsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThr 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 GAAGGGAACAACATCAGCCTCACTTGCATAGCCACAGGTAGGCCGGAGCCTACAGTAACC 504

Qy        169 TrpArgHisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIle 188
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Db        505 TGGAGACATATTTCTCCCAAGGCCGTTGGCTTTGTGAGTGAGGATGAGTACCTGCAGATC 564

Qy        189 GlnGlyIleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAla 208
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Db        565 CAGGGCATCACTCGGGAACAGTCAGGCGAGTACGAGTGCAGCGCCTCCAACGACGTGGCG 624

Qy        209 AlaProValValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAla 228
              ||||||||||||  ||||||||||||||||||||||||||||||||||  ||||||||||
Db        625 GCACCAGTGGTACCAAGAGTGAAGGTCACCGTGAACTATCCACCATACTTCTCAGAAGCT 684

Qy        229 LysGlyThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaVal 248
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 AAGGGCACAGGTGTCCCCGTGGGGCAGAAGGGGACTCTGCAGTGTGAAGCTTCCGCAGTC 744

Qy        249 ProSerAlaGluPheGlnTrpTyrLysAspAspLysArgLeuIleGluGlyLysLysGly 268
                ||||||||||||||||||||||::::||||||||||||||||||:::||||||||||||||||||
Db        745 CCTTCAGCAGAATTTCAATGGTTCAAGGATGACAAAAGACTGGTCGAAGGAAAGAAGGGA 804

Qy        269 ValLysValGluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHis 288
                ||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db        805 GTCAAAGTGGAAAACAGACCTTTCCTTTCAAAACTCACCTTTTTCAACGTCTCTGAACAT 864

Qy        289 AspTyrGlyAsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIle 308
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Db        865 GACTATGGGAACTACACATGTGTGGCCTCCAACAAGCTGGGTCACACCAACGCCAGCATC 924

Qy        309 MetLeuPheGlyProGlyAlaValSerGluValSerAsnGlyThrSerArgArgAlaGly 328
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Db        925 ATGCTATTTGGTCCCGGTGCTGTCAGTGAGGTCAACAATGGGACATCAAGGAGGGCAGGC 984

Qy        329 CysValTrpLeuLeuProLeuLeuValLeuHisLeuLeuLeuLysPhe 344
                |||:::|||||||||||||||||||||||||||||||||||||||||||
Db        985 TGCATTTGGCTCCTCCCTCTTCTGGTCTTACACCTGCTCCTCAAATTT 1032

RESULT 15
BC050716
LOCUS       BC050716                1325 bp    mRNA    linear   PRI 22-APR-2003
DEFINITION  Homo sapiens mRNA similar to neurotrimin (cDNA clone MGC:60329
            IMAGE:6166839), complete cds.
ACCESSION   BC050716
VERSION     BC050716.1  GI:30047134
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1325)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
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            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
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            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1325)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-APR-2003) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 110 Row: m Column: 8
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 7705412.
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BASE COUNT     398 a    295 c    375 g    257 t
ORIGIN

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Score:                  1500.50         Matches:        290
Percent Similarity:     97.02%          Conservative:   3
Best Local Similarity:  96.03%          Mismatches:     8
Query Match:            83.08%          Indels:         2
DB:                     9               Gaps:           1

US-10-017-084A-523 (1-344) x BC050716 (1-1325)

Qy         11 SerIleSerTrpAlaIlePheThrGlyLeuAlaAlaLeuCysLeuPheGlnGlyValPro 30
               |||   ||||||:::      :::|||     :::|||           |||||||||
Db         49 AGTGCCTCGTGGTCGTGTCTCTCAGGCTGCTGTTCCTTG---TACCC-ACAGGAGTGCCC 104

Qy         31 ValArgSerGlyAspAlaThrProLysAlaMetAspAsnValThrValArgGlnGly 50
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Db        105 GTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGG 164

Qy         51 GluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsn 70
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         71 ArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeu 90
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Db        225 CGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTT 284

Qy         91 LeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyrAspGlu 110
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 CTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAG 344

Qy        111 GlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeu 130
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 GGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTC 404

Qy        131 IleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGly 150
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        151 AsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArg 170
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Db        465 AACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGA 524

Qy        171 HisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGly 190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 CACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGC 584

Qy        191 IleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaPro 210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCC 644

Qy        211 ValValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGly 230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGT 704

Qy        231 ThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSer 250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        705 ACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCA 764

Qy        251 AlaGluPheGlnTrpTyrLysAspAspLysArgLeuIleGluGlyLysLysGlyValLys 270
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Db        765 GCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAA 824

Qy        271 ValGluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyr 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        825 GTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTAT 884

Qy        291 GlyAsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeu 310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        885 GGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTA 944

Qy        311 PheGly 312
              ||||||
Db        945 TTTGGT 950
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Search completed: September 11, 2003, 04:30:29
Job time : 4595 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 11, 2003, 03:05:48 ; Search time 359 Seconds
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Title: US-10-017-084A-523
Perfect score: 1806
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Searched: 2552756 seqs, 1349719017 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10017084/runat_09092003_141325_21860/app_query.fasta_1.519
-DB=N_Geneseq_19Jun03 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10017084_@CGN_1_1_490_@runat_09092003_141325_21860 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_19Jun03:*
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24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1806	100.0	1032	21	AAZ47892	Human protein enco
2	1806	100.0	1679	20	AAZ34324	Human PRO337 nucle
3	1806	100.0	1679	21	AAC78590	Human PRO337 nucle
4	1806	100.0	1679	22	AAS21431	Human cDNA sequenc
5	1806	100.0	1679	22	AAC87037	Nucleotide sequenc
6	1806	100.0	1679	24	ABL95588	Human angiogenesis
7	1806	100.0	1679	24	ABL88099	Human PRO337 cDNA
8	1806	100.0	1679	24	ABK33598	cDNA encoding huma
9	1806	100.0	1679	25	ACA60526	Novel human secret
10	1806	100.0	1679	25	ACA03790	cDNA encoding huma
11	1806	100.0	1679	25	ACA04211	Human cDNA encodin
12	1806	100.0	1679	25	ACA04516	Novel human secret
13	1806	100.0	1679	25	ACA04996	Novel human secret
14	1806	100.0	1679	25	ABX89328	DNA encoding novel
15	1806	100.0	1679	25	ABX92696	cDNA encoding huma
16	1806	100.0	1693	21	AAZ47893	Human protein enco
17	1799	99.6	1603	21	AAA88790	Human SECX cDNA Cl
18	1799	99.6	2012	21	AAA88791	Human SECX cDNA Cl
19	1756	97.2	1873	24	ABK49272	Human Kruppel asso
20	1752	97.0	1690	22	AAI59655	Human polynucleoti
21	1665.5	92.2	1678	22	AAI57869	Human polynucleoti
22	1665.5	92.2	1839	25	ABX76448	Lung cancer-associ
23	1642	90.9	939	21	AAZ47894	Human protein enco
24	1286.5	71.2	3069	14	AAQ51015	Rat opioid recepto
25	1260	69.8	2179	14	AAQ51017	Rat opioid recepto
26	1259	69.7	2337	14	AAQ51016	Rat opioid recepto
27	1173	65.0	832	21	AAA44536	Human secreted exp
28	932.5	51.6	1411	24	AAL50356	Human limbic syste
29	931.5	51.6	1195	25	ABX63560	Human cDNA #560 di
30	926.5	51.3	1014	17	AAT42081	Rat LAMP coding se
31	926.5	51.3	1238	17	AAT42080	Rat LAMP coding se
32	923.5	51.1	977	17	AAT42079	Human LAMP residue
33	913	50.6	1307	17	AAT42116	Rat LAMP clone 6c
34	908	50.3	924	17	AAT42084	Human LAMP residue
35	907	50.2	945	17	AAT42085	Rat LAMP residues
36	905	50.1	930	17	AAT42083	Rat mature LAMP co
37	902	49.9	912	17	AAT42082	Human mature LAMP
38	893	49.4	1757	25	ABZ76264	Human GENSET cDNA
39	886.5	49.1	861	17	AAT42086	Human LAMP residue
40	885.5	49.0	861	17	AAT42087	Rat LAMP residues
41	885	49.0	1153	22	AAH34425	Human colon cancer
42	859	47.6	503	20	AAZ34325	Human EST DNA42301
43	859	47.6	503	21	AAC78591	Human EST DNA42301
44	859	47.6	503	25	ABX92697	Human PRO337 EST p
45	823	45.6	1196	24	ABQ82337	Human NOV12a encod

ALIGNMENTS

RESULT 1
AAZ47892
ID AAZ47892 standard; cDNA; 1032 BP.
XX
AC AAZ47892;
XX
DT 10-MAR-2000 (first entry)
XX
DE Human protein encoding cDNA SEQ ID NO:2.
XX
KW Human; haematopoietic cell regulation; tissue generation; reparation;
KW activin; inhibin; taxis; chemotaxis; blood coagulation; thrombus;
KW receptor; ligand; autoimmune; infection-related immunodeficiency;
KW inflammatory disorder; neurological disease; ss.
XX
OS Homo sapiens.
XX

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FH   Key             Location/Qualifiers
FT   CDS             1..1032
FT                   /*tag=  a
FT                   /note= "no stop codon given"
XX
PN   WO9958668-A1.
XX
PD   18-NOV-1999.
XX
PF   13-MAY-1999;   99WO-JP02485.
XX
PR   14-MAY-1998;   98JP-0131815.
XX
PA   (ONOY ) ONO PHARM CO LTD.
XX
PI   Fukushima D,  Shibayama S,  Tada H;
XX
DR   WPI; 2000-062298/05.
DR   P-PSDB; AAY57601.
XX
PT   New polypeptides of human origin having cell regulatory, tissue
PT   generation, coagulant and other activities
XX
PS   Claim 4; Page 41; 84pp; Japanese.
XX
CC   The present sequence encodes a specifically claimed novel human protein.
CC   The novel human protein can be used in therapeutic drugs for the
CC   prevention and treatment of a broad range of disorders including
CC   autoimmune and infection-related immunodeficiency, inflammatory
CC   disorders, and neurological diseases. The novel protein is expected of
CC   having haematopoietic cell regulatory activity, tissue generation/
CC   reparation activity, activin/inhibin activity, taxis/chemotaxis activity,
CC   blood coagulation and thrombus activity, and receptor/ligand activity.
XX
SQ   Sequence 1032 BP; 267 A; 281 C; 270 G; 214 T; 0 other;

Alignment Scores:
Pred..No.:              4.46e-167      Length:         1032
Score:                  1806.00        Matches:        344
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     21             Gaps:           0

US-10-017-084A-523 (1-344) x AAZ47892 (1-1032)

Qy          1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
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Db          1 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 60

Qy         21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
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Db         61 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 120

Qy         41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
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Db        121 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 180

Qy         61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
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Db        181 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 240

Qy         81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
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Db        241 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 300

Qy        101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
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Db        301 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 360

Qy        121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
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Db        361 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 420

Qy        141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
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Db        421 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 480

Qy        161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
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Qy        181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
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Qy        201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
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Qy        221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
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Qy        241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
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Qy        261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
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Db        781 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 840

Qy        281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
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Qy        301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
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Qy        321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
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Db        961 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1020

Qy        341 LeuLeuLysPhe 344
              ||||||||||||
Db       1021 CTTCTCAAATTT 1032

RESULT 2
AAZ34324
ID   AAZ34324 standard; cDNA; 1679 BP.
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AC   AAZ34324;
XX
DT   07-DEC-1999  (first entry)
XX
DE   Human PRO337 nucleotide sequence.
XX
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KW   probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW   secreted protein; transmembrane protein; ss.
XX
OS   Homo sapiens.
XX
PN   WO9946281-A2.
XX
PD   16-SEP-1999.
XX
PF   08-MAR-1999;   99WO-US05028.
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PR   12-MAR-1998;   98US-0077791.
PR   13-MAR-1998;   98US-0078004.
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PR 17-MAR-1998; 98US-0040220.
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PR 20-MAR-1998; 98US-0078910.
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PR 01-APR-1998; 98US-0080327.
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PR 15-APR-1998; 98US-0081955.
PR 21-APR-1998; 98US-0082568.
PR 21-APR-1998; 98US-0082569.
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PR 29-APR-1998; 98US-0083558.
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PR 05-MAY-1998; 98US-0084366.
PR 06-MAY-1998; 98US-0084414.
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PR 07-MAY-1998; 98US-0084640.
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PR 13-MAY-1998; 98US-0085323.
PR 13-MAY-1998; 98US-0085338.
PR 13-MAY-1998; 98US-0085339.
PR 15-MAY-1998; 98US-0085573.
PR 15-MAY-1998; 98US-0085579.
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PR 15-MAY-1998; 98US-0085704.
PR 18-MAY-1998; 98US-0086023.
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PR 28-MAY-1998; 98US-0087098.
PR 28-MAY-1998; 98US-0087106.
PR 28-MAY-1998; 98US-0087208.
PR 30-JUL-1998; 98US-0094651.
PR 11-SEP-1998; 98US-0100038.
XX
PA (GETH) GENENTECH INC.
XX
PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX
DR WPI; 1999-551358/46.
DR P-PSDB; AAY41773.
XX
PT New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders
XX
PS Claim 2; Fig 221; 530pp; English.
XX
CC The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as
CC sources of probes, primers, for chromosome mapping, and for generation
CC of antisense sequences. They can also be used to create transgenic
CC animals. The proteins can be used to treat a variety of diseases and
CC disorders, depending on their function. Diseases that may be treated
CC include blood coagulation disorders, cancers and cellular adhesion
CC disorders. They may also be used to raise antibodies. AAZ33891 to
CC AAZ34338, and AAY41685 to AAY41774 represent polynucleotide and
CC polypeptide sequence given in the exemplification of the present
CC invention.
XX
SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

Alignment Scores:

Pred. No.:	8.55e-167	Length:	1679
Score:	1806.00	Matches:	344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	20	Gaps:	0

US-10-017-084A-523 (1-344) x AAZ34324 (1-1679)

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Qy          1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
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Db        134 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 193

Qy         21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        194 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 253

Qy         41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        254 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 313

Qy         61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
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Db        314 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 373

Qy         81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 433

Qy        101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493

Qy        121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        494 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 553

Qy        141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
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Db        554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613

Qy        161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673

Qy        181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy        201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy        221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853

Qy        241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        854 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 913

Qy        261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 973

Qy        281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

Qy        301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1093

Qy        321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1153

Qy        341 LeuLeuLysPhe 344
              ||||||||||||
Db       1154 CTTCTCAAATTT 1165
```

RESULT 3
AAC78590
ID AAC78590 standard; cDNA; 1679 BP.
XX
AC AAC78590;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human PRO337 nucleotide sequence SEQ ID NO:522.
XX
KW Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
KW expressed sequence tag; detection; cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200053756-A2.
XX
PD 14-SEP-2000.
XX
PF 18-FEB-2000; 2000WO-US04341.
XX
PR 08-MAR-1999; 99WO-US05028.
PR 12-MAR-1999; 99US-0123957.
PR 29-MAR-1999; 99US-0126773.
PR 21-APR-1999; 99US-0130232.
PR 28-APR-1999; 99US-0131445.
PR 14-MAY-1999; 99US-0134287.
PR 23-JUN-1999; 99US-0141037.
PR 26-JUL-1999; 99US-0145698.
PR 29-OCT-1999; 99US-0162506.
PR 30-NOV-1999; 99WO-US28313.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2000-611443/58.
DR P-PSDB; AAB44329.
XX
PT Novel PRO polypeptides and polynucleotides used in detection methods,
PT to target bioactive molecules to specific cells, and to modulate
PT cellular activities -
XX
PS Claim 2; Fig 221; 636pp; English.
XX
CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed
CC sequence tag) sequences which encode secreted or transmembrane PRO
CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic
CC activity. The polynucleotides and polypeptides can be used for detecting
CC the presence of PRO polypeptides in samples, for linking bioactive
CC molecules to cells and for modulating biological activities of cells,
CC using the polypeptides for specific targeting. The polypeptide targeting
CC can be used to kill the target cells, e.g. for the treatment of cancers.
CC The polypeptide pairs provide specific targeting of bioactive molecules
CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
CC the isolation of the PRO polynucleotide sequences.
XX
SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

Alignment Scores:

Pred. No.:	8.55e-167	Length:	1679
Score:	1806.00	Matches:	344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	21	Gaps:	0

US-10-017-084A-523 (1-344) x AAC78590 (1-1679)

```
Qy          1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 193

Qy         21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        194 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 253

Qy         41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        254 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 313

Qy         61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        314 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 373

Qy         81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 433
```

```
Qy        101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493

Qy        121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        494 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 553

Qy        141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613

Qy        161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673

Qy        181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy        201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy        221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853

Qy        241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        854 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 913

Qy        261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 973

Qy        281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

Qy        301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1093

Qy        321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1153

Qy        341 LeuLeuLysPhe 344
              ||||||||||||
Db       1154 CTTCTCAAATTT 1165
```

RESULT 4
AAS21431
ID AAS21431 standard; cDNA; 1679 BP.
XX
AC AAS21431;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human cDNA sequence encoding for PRO337 polypeptide.
XX
KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KW adipocyte; A-peptide; factor VIIA; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN WO200140466-A2.
XX
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-US32678.
XX
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 09-DEC-1999; 99US-0170262.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 30-DEC-1999; 99WO-US31243.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 10-NOV-2000; 2000WO-US30873.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2001-408281/43.
DR P-PSDB; AAU12359.
XX
PT Isolated, secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing
PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
PT lung, breast, prostate, cervical
XX
PS Claim 3; Fig 375; 813pp; English.
XX
CC AAS21244-AAS21518 encode for novel human secretory and transmembrane
CC PRO polypeptides. The PRO polypeptides are useful to detect other
CC PRO polypeptides, to link bioactive molecules to cells expressing
CC PRO polypeptides, to modulate biological activities of cells expressing
CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample.
CC Some of the 275 sequences are also useful to stimulate the release of
CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
CC proliferation or differentiation of chondrocytes, the proliferation or
CC gene expression in pericyte cells, the release of proteoglycans from
CC cartilage, the proliferation of inner ear utricular supporting cells or
CC of T-lymphocytes, the release of a cytokine from peripheral blood
CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
CC to factor VIIA. The PRO polypeptides can be used in assays to identify
CC molecules involved in binding interactions. The polynucleotides encoding
CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy.
XX
SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

Alignment Scores:
Pred. No.: 8.55e-167 Length: 1679
Score: 1806.00 Matches: 344

```
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            100.00%       Indels:        0
DB:                     22            Gaps:          0

US-10-017-084A-523 (1-344) x AAS21431 (1-1679)

Qy          1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 193

Qy         21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        194 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 253

Qy         41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        254 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 313

Qy         61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        314 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 373

Qy         81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 433

Qy        101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493

Qy        121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        494 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 553

Qy        141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613

Qy        161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673

Qy        181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy        201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy        221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853

Qy        241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        854 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 913

Qy        261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 973

Qy        281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

Qy        301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1093

Qy        321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db       1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1153

Qy        341 LeuLeuLysPhe 344
              ||||||||||||
Db       1154 CTTCTCAAATTT 1165

RESULT 5
AAC87037
ID   AAC87037 standard; cDNA; 1679 BP.
XX
AC   AAC87037;
XX
DT   20-APR-2001  (first entry)
XX
DE   Nucleotide sequence of human polypeptide PRO337.
XX
KW   Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;
KW   PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO1308;
KW   PRO1183; PRO1272; PRO1419; PRO4999; PRO7170; PRO248; PRO353; PRO1318;
KW   PRO1600; PRO9940; PRO533; PRO301; PRO187; PRO337; PRO1411; PRO4356;
KW   PRO246; PRO265; PRO941; PRO10096; PRO6003; PRO6004; PRO350; PRO2630;
KW   PRO6309; cell death; genetic disorder; transgenic animal; gene therapy;
KW   ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             134..1168
FT                   /*tag=  a
FT   sig_peptide     134..216
FT                   /*tag=  b
XX
PN   WO200077037-A2.
XX
PD   21-DEC-2000.
XX
PF   22-MAY-2000; 2000WO-US14042.
XX
PR   15-JUN-1999;   99US-0139695.
PR   20-JUL-1999;   99US-0145070.
PR   26-JUL-1999;   99US-0145698.
PR   17-AUG-1999;   99US-0149396.
PR   01-SEP-1999;   99WO-US20111.
PR   08-SEP-1999;   99WO-US20594.
PR   15-SEP-1999;   99WO-US21090.
PR   15-SEP-1999;   99WO-US21547.
PR   30-NOV-1999;   99WO-US28313.
PR   01-DEC-1999;   99WO-US28301.
PR   02-DEC-1999;   99WO-US28565.
PR   07-DEC-1999;   99US-0169495.
PR   05-JAN-2000; 2000WO-US00219.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   22-FEB-2000; 2000WO-US04414.
PR   01-MAR-2000; 2000WO-US05601.
PR   02-MAR-2000; 2000WO-US05841.
PR   20-MAR-2000; 2000WO-US07377.
PR   30-MAR-2000; 2000WO-US08439.
PR   15-MAY-2000; 2000WO-US13358.
PR   17-MAY-2000; 2000WO-US13705.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Botstein DA,  Desnoyers L,  Eaton DL;
PI   Ferrara N,  Fong S,  Gao W,  Gerber H,  Gerritsen ME,  Goddard A;
PI   Godowski PJ,  Gurney AL,  Kljavin IJ,  Mather JP,  Napier MA,  Pan J;
PI   Paoni NF,  Roy MA,  Stewart TA,  Tumas D,  Watanabe CK,  Williams PM;
PI   Wood WI,  Zhang Z;
XX
DR   WPI; 2001-050091/06.
DR   P-PSDB; AAB31204.
XX
PT   Isolated nucleic acid molecule encoding a PRO polypeptide which is a
```

```
PT   transmembrane polypeptide is useful for gene therapy and identification
PT   of related polypeptides -
XX
PS   Claim 2; Fig 51; 244pp; English.
XX
CC   The present sequence encodes a human secreted and transmembrane
CC   polypeptide. The specification describes human polypeptides, designated
CC   PRO196, PRO444, PRO183, PRO185, PRO210, PRO215, PRO217, PRO242, PRO288,
CC   PRO365, PRO1361, PRO1308, PRO1183, PRO1272, PRO1419, PRO4999, PRO7170,
CC   PRO248, PRO353, PRO1318, PRO1600, PRO9940, PRO533, PRO301, PRO187,
CC   PRO337, PRO1411, PRO4356, PRO246, PRO265, PRO941, PRO10096, PRO6003,
CC   PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of cells
CC   can be modulated with agents that bind to these polypeptides, resulting
CC   in the death of the cells. The polynucleotides encoding these
CC   polypeptides are useful in the recombinant production of the
CC   polypeptides, as a hybridisation probe to screen libraries to isolate
CC   homologous sequences, or to map the gene. They may also be used for
CC   analysing genetic disorders, and to produce transgenic animals which are
CC   useful for the development and screening of therapeutically useful
CC   reagents. The polynucleotides can also be used in gene therapy e.g. to
CC   replace a defective gene.
XX
SQ   Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

Alignment Scores:
Pred. No.:              8.55e-167       Length:         1679
Score:                  1806.00         Matches:        344
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     22              Gaps:           0

US-10-017-084A-523 (1-344) x AAC87037 (1-1679)

Qy          1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 193

Qy         21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        194 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 253

Qy         41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        254 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 313

Qy         61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        314 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 373

Qy         81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 433

Qy        101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493

Qy        121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        494 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 553

Qy        141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613

Qy        161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673

Qy        181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy        201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy        221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853

Qy        241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        854 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 913

Qy        261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 973

Qy        281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

Qy        301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1093

Qy        321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1153

Qy        341 LeuLeuLysPhe 344
              ||||||||||||
Db       1154 CTTCTCAAATTT 1165

RESULT 6
ABL95588
ID   ABL95588 standard; cDNA; 1679 BP.
XX
AC   ABL95588;
XX
DT   19-JUL-2002  (first entry)
XX
DE   Human angiogenesis related cDNA PRO337 SEQ ID NO: 55.
XX
KW   Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW   atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW   cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;
KW   antiarteriosclerotic; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200208284-A2.
XX
PD   31-JAN-2002.
XX
PF   09-JUL-2001; 2001WO-US21735.
XX
PR   20-JUL-2000; 2000US-219556P.
PR   25-JUL-2000; 2000US-220624P.
PR   25-JUL-2000; 2000US-220664P.
PR   28-JUL-2000; 2000WO-US20710.
PR   02-AUG-2000; 2000US-222695P.
PR   17-AUG-2000; 2000US-0643657.
PR   23-AUG-2000; 2000WO-US23522.
PR   24-AUG-2000; 2000WO-US23328.
PR   07-SEP-2000; 2000US-230978P.
PR   15-SEP-2000; 2000US-000000P.
PR   18-SEP-2000; 2000US-0664610.
PR   18-SEP-2000; 2000US-0665350.
PR   24-OCT-2000; 2000US-242922P.
PR   08-NOV-2000; 2000US-0709238.
PR   08-NOV-2000; 2000WO-US30952.
PR   10-NOV-2000; 2000WO-US30873.
PR   01-DEC-2000; 2000WO-US32678.
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PR   20-DEC-2000; 2000US-0747259.
PR   20-DEC-2000; 2000WO-US34956.
PR   22-JAN-2001; 2001US-0767609.
PR   28-FEB-2001; 2001US-0796498.
PR   28-FEB-2001; 2001WO-US06520.
PR   01-MAR-2001; 2001WO-US06666.
PR   09-MAR-2001; 2001US-0802706.
PR   14-MAR-2001; 2001US-0808689.
PR   22-MAR-2001; 2001US-0816744.
PR   05-APR-2001; 2001US-0828366.
PR   10-MAY-2001; 2001US-0854208.
PR   10-MAY-2001; 2001US-0854280.
PR   25-MAY-2001; 2001US-0866028.
PR   25-MAY-2001; 2001US-0866034.
PR   25-MAY-2001; 2001WO-US17092.
PR   30-MAY-2001; 2001US-0870574.
PR   30-MAY-2001; 2001WO-US17443.
PR   01-JUN-2001; 2001WO-US17800.
PR   20-JUN-2001; 2001WO-US19692.
PR   28-JUN-2001; 2001WO-US00000.
XX
PA   (GETH ) GENENTECH INC.
PA   (BAKE/) BAKER K P.
PA   (FERR/) FERRARA N.
PA   (GERB/) GERBER H.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (HILL/) HILLAN K J.
PA   (MARS/) MARSTERS S A.
PA   (PANJ/) PAN J.
PA   (PAON/) PAONI N F.
PA   (STEP/) STEPHAN J F.
PA   (WATA/) WATANABE C K.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
XX
PI   Baker KP,  Ferrara N,  Gerber H,  Gerritsen ME,  Goddard A;
PI   Godowski PJ,  Gurney AL,  Hillan KJ,  Marsters SA,  Pan J,  Paoni NF;
PI   Stephan JF,  Watanabe CK,  Williams PM,  Wood WI,  Ye W;
XX
DR   WPI; 2002-171999/22.
DR   P-PSDB; ABB95450.
XX
PT   One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT   useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT   infarction), endothelial or angiogenic disorders in a mammal
XX
PS   Claim 1; Fig 55; 567pp; English.
XX
CC   The present invention provides the protein and coding sequences of human
CC   PRO proteins. These are useful for treating or diagnosing a
CC   cardiovascular, endothelial or angiogenic disorder, including cardiac
CC   hypertrophy, trauma, cancer, age-related macular degeneration,
CC   atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC   angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC   angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC   healing. The present sequence is a coding sequence of the invention.
XX
SQ   Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

Alignment Scores:
Pred. No.:                8.55e-167      Length:          1679
Score:                    1806.00        Matches:         344
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       24             Gaps:            0

US-10-017-084A-523 (1-344) x ABL95588 (1-1679)

Qy          1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20

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Db        134 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 193

Qy         21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        194 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 253

Qy         41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        254 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 313

Qy         61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        314 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 373

Qy         81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 433

Qy        101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493

Qy        121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        494 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 553

Qy        141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613

Qy        161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673

Qy        181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy        201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy        221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853

Qy        241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        854 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 913

Qy        261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 973

Qy        281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

Qy        301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1093

Qy        321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1153

Qy        341 LeuLeuLysPhe 344
                 ||||||||||||
Db       1154 CTTCTCAAATTT 1165

RESULT 7
ABL88099
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ID   ABL88099 standard; cDNA; 1679 BP.
XX
AC   ABL88099;
XX
DT   16-MAY-2002  (first entry)
XX
DE   Human PRO337 cDNA sequence SEQ ID NO:55.
XX
KW   Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
KW   vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW   gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KW   angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW   age-related macular degeneration; arterial restenosis; angina;
KW   rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW   lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW   wound healing; chromosome mapping; gene mapping; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200200690-A2.
XX
PD   03-JAN-2002.
XX
PF   20-JUN-2001; 2001WO-US19692.
XX
PR   23-JUN-2000; 2000US-213637P.
PR   20-JUL-2000; 2000US-219556P.
PR   25-JUL-2000; 2000US-220624P.
PR   25-JUL-2000; 2000US-220664P.
PR   28-JUL-2000; 2000WO-US20710.
PR   02-AUG-2000; 2000US-222695P.
PR   17-AUG-2000; 2000US-0643657.
PR   23-AUG-2000; 2000WO-US23522.
PR   24-AUG-2000; 2000WO-US23328.
PR   07-SEP-2000; 2000US-230978P.
PR   18-SEP-2000; 2000US-0664610.
PR   18-SEP-2000; 2000US-0665350.
PR   24-OCT-2000; 2000US-242922P.
PR   08-NOV-2000; 2000US-0709238.
PR   08-NOV-2000; 2000WO-US30952.
PR   10-NOV-2000; 2000WO-US30873.
PR   01-DEC-2000; 2000WO-US32678.
PR   20-DEC-2000; 2000US-0747259.
PR   20-DEC-2000; 2000WO-US34956.
PR   22-JAN-2001; 2001US-0767609.
PR   28-FEB-2001; 2001US-0796498.
PR   28-FEB-2001; 2001WO-US06520.
PR   01-MAR-2001; 2001WO-US06666.
PR   09-MAR-2001; 2001US-0802706.
PR   14-MAR-2001; 2001US-0808689.
PR   22-MAR-2001; 2001US-0816744.
PR   05-APR-2001; 2001US-0828366.
PR   10-MAY-2001; 2001US-0854208.
PR   10-MAY-2001; 2001US-0854280.
PR   25-MAY-2001; 2001US-0866028.
PR   25-MAY-2001; 2001US-0866034.
PR   25-MAY-2001; 2001WO-US17092.
PR   30-MAY-2001; 2001US-0870574.
PR   30-MAY-2001; 2001WO-US17443.
PR   01-JUN-2001; 2001WO-US17800.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Ferrara N,  Gerber H,  Gerritsen ME,  Goddard A;
PI   Godowski PJ,  Gurney AL,  Hillan KJ,  Marsters SA,  Pan J,  Paoni NF;
PI   Stephan JF,  Watanabe CK,  Williams PM,  Wood WI,  Ye W;
XX
DR   WPI; 2002-090516/12.
DR   P-PSDB; ABB84844.
XX
PT   One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT   useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT   infarction), endothelial or angiogenic disorders in a mammal -
XX
PS   Claim 2; Fig 55; 565pp; English.
XX
CC   ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC   ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
CC   antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
CC   activities, and can be used in gene therapy. The PRO polynucleotides,
CC   proteins, agonists and antagonists are useful for treating or diagnosing
CC   a cardiovascular, endothelial or angiogenic disorder in a mammal,
CC   e.g. cardiac hypertrophy, trauma, cancer, age-related macular
CC   degeneration, atherosclerosis, hypertension, arterial restenosis,
CC   rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
CC   lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
CC   carcinoma) and wound healing. The PRO polynucleotides have applications
CC   in molecular biology, including use as hybridisation probes, and in
CC   chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
CC   probes used in the exemplification of the present invention.
XX
SQ   Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

Alignment Scores:
Pred. No.:                8.55e-167       Length:          1679
Score:                    1806.00         Matches:         344
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       24              Gaps:            0

US-10-017-084A-523 (1-344) x ABL88099 (1-1679)

Qy          1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 193

Qy         21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        194 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 253

Qy         41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        254 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 313

Qy         61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        314 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 373

Qy         81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 433

Qy        101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493

Qy        121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        494 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 553

Qy        141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613

Qy        161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673

Qy        181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy        201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793
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Qy        221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853

Qy        241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        854 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 913

Qy        261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 973

Qy        281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

Qy        301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1093

Qy        321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1153

Qy        341 LeuLeuLysPhe 344
              ||||||||||||
Db       1154 CTTCTCAAATTT 1165
```

RESULT 8
ABK33598

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ID   ABK33598 standard; cDNA; 1679 BP.
XX
AC   ABK33598;
XX
DT   08-MAY-2002  (first entry)
XX
DE   cDNA encoding human PRO protein, Seq ID No 125.
XX
KW   Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW   breast cancer; prostate tumour; rectal tumour; liver tumour;
KW   pericyte cell proliferation; chondrocyte cell proliferation;
KW   tumour necrosis factor-alpha; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200208288-A2.
XX
PD   31-JAN-2002.
XX
PF   29-JUN-2001; 2001WO-US21066.
XX
PR   20-JUL-2000; 2000US-219556P.
PR   25-JUL-2000; 2000US-220585P.
PR   25-JUL-2000; 2000US-220605P.
PR   25-JUL-2000; 2000US-220607P.
PR   25-JUL-2000; 2000US-220624P.
PR   25-JUL-2000; 2000US-220638P.
PR   25-JUL-2000; 2000US-220664P.
PR   25-JUL-2000; 2000US-220666P.
PR   26-JUL-2000; 2000US-220893P.
PR   28-JUL-2000; 2000WO-US20710.
PR   23-AUG-2000; 2000WO-US23522.
PR   24-AUG-2000; 2000WO-US23328.
PR   15-SEP-2000; 2000US-000000P.
PR   10-NOV-2000; 2000WO-US30873.
PR   28-NOV-2000; 2000US-253646P.
PR   01-DEC-2000; 2000WO-US32678.
PR   20-DEC-2000; 2000US-0747259.
PR   20-DEC-2000; 2000WO-US34956.
PR   28-FEB-2001; 2001WO-US06520.
PR   10-MAY-2001; 2001US-0854280.
PR   25-MAY-2001; 2001WO-US17092.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Desnoyers L,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi JC,  Gurney AL,  Smith V,  Stephan JF,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2002-172001/22.
DR   P-PSDB; AAU83654.
XX
PT   One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT   useful for treating a PRO related disorder and for diagnosing tumours
PT   such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
PT   tumour or liver tumour -
XX
PS   Claim 2; Figure 125; 359pp; English.
XX
CC   The invention relates to one hundred and twenty two nucleic acids
CC   encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
CC   encode human secreted proteins. The PRO nucleic acids, polypeptides,
CC   agonists and antagonists are useful for treating a PRO related disorder.
CC   The PRO polypeptides are useful for diagnosing tumours, especially lung
CC   cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
CC   liver tumour. The PRO polypeptides are useful for stimulating the
CC   proliferation of, or gene expression, in pericyte cells, for stimulating
CC   the proliferation or differentiation of chondrocyte cells, for
CC   stimulating the release of tumour necrosis factor-alpha from human blood,
CC   for stimulating or inhibiting the proliferation of normal human dermal
CC   fibroblast cells. The PRO polypeptide may also be used as molecular
CC   weight markers and for tissue typing. The PRO nucleic acids have
CC   applications in molecular biology, including use as hybridisation probes,
CC   and in chromosome and gene mapping. ABK33536-ABK33657 represent human
CC   PRO protein coding sequences of the invention.
XX
SQ   Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;
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Alignment Scores:

Pred. No.:	8.55e-167	Length:	1679
Score:	1806.00	Matches:	344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-10-017-084A-523 (1-344) x ABK33598 (1-1679)

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Qy          1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 193

Qy         21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        194 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 253

Qy         41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        254 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 313

Qy         61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        314 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 373

Qy         81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 433

Qy        101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493

Qy        121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        494 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 553
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```
Qy       141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613

Qy       161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673

Qy       181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy       201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy       221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853

Qy       241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       854 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 913

Qy       261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 973

Qy       281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

Qy       301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1093

Qy       321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1153

Qy       341 LeuLeuLysPhe 344
            ||||||||||||
Db      1154 CTTCTCAAATTT 1165
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RESULT 9
ACA60525
ID ACA60525 standard; cDNA; 1679 BP.
XX
AC ACA60526;
XX
DT 11-JUN-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO337 cDNA.
XX
KW Human; secreted and transmembrane polypeptide; PRO;
KW fibroblast growth factor receptor; PRO533; PRO301; PRO187; PRO337;
KW PRO1411; PRO10096; PRO246; PRO6307; PRO6003; FGFR-3; FGFR-4; FGFR-1;
KW FGFR-2; PRO6004; PRO4356; PRO2630; PRO265; PRO951; bioactive molecule;
KW toxin; radiolabel; antibody; cell death; chromosome mapping;
KW gene mapping; transgenic animal; knockout animal; gene therapy;
KW tissue typing; gene; ss.
XX
OS Homo sapiens.
XX
PN US2002177165-A1.
XX
PD 28-NOV-2002.
XX
PF 01-FEB-2002; 2002US-0066500.
XX
PR 14-JUL-1998; 98WO-US14552.
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19093.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 20-NOV-1998; 98WO-US24855.
PR 25-NOV-1998; 98WO-US25190.
PR 01-DEC-1998; 98WO-US25108.
PR 08-MAR-1999; 99WO-US05028.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28565.
PR 20-DEC-1999; 99WO-US30999.
PR 05-JAN-2000; 2000WO-US00219.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 09-MAR-2000; 2000WO-US06471.
PR 20-MAR-2000; 2000WO-US07377.
PR 30-MAR-2000; 2000WO-US08439.
PR 15-MAY-2000; 2000WO-US13358.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 01-DEC-2000; 2000WO-US32678.
PR 28-FEB-2001; 2001WO-US06520.
PR 30-MAY-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 26-AUG-1997; 97US-056974P.
PR 17-SEP-1997; 97US-059115P.
PR 18-SEP-1997; 97US-059263P.
PR 19-SEP-1997; 97US-059588P.
PR 17-OCT-1997; 97US-062285P.
PR 24-OCT-1997; 97US-062816P.
PR 24-OCT-1997; 97US-063082P.
PR 27-OCT-1997; 97US-063329P.
PR 29-OCT-1997; 97US-063733P.
PR 21-NOV-1997; 97US-066364P.
PR 25-NOV-1997; 97US-066840P.
PR 16-DEC-1997; 97US-069694P.
PR 09-FEB-1998; 98US-074086P.
PR 09-FEB-1998; 98US-074092P.
PR 25-MAR-1998; 98US-079294P.
PR 08-APR-1998; 98US-081049P.
PR 10-AUG-1998; 98US-095998P.
PR 18-AUG-1998; 98US-097000P.
PR 09-SEP-1998; 98US-099601P.
PR 10-SEP-1998; 98US-099803P.
PR 10-SEP-1998; 98US-099811P.
PR 10-SEP-1998; 98US-099812P.
PR 17-SEP-1998; 98US-100858P.
PR 24-SEP-1998; 98US-101922P.
PR 28-OCT-1998; 98US-106032P.
PR 20-NOV-1998; 98US-109304P.
PR 23-MAR-1999; 99US-125778P.
PR 15-JUN-1999; 99US-139695P.
PR 20-JUL-1999; 99US-145070P.
PR 26-JUL-1999; 99US-145698P.
PR 17-AUG-1999; 99US-149396P.
PR 07-DEC-1999; 99US-169495P.
PR 15-NOV-2001; 2001US-0002796.
XX

```
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Botstein DA,  Desnoyers L,  Eaton DL;
PI   Ferrara N,  Fong S,  Gao W,  Gerber H,  Gerritsen ME,  Goddard A;
PI   Godowski PJ,  Gurney AL,  Kljavin IJ,  Mather JP,  Napier MA,  Pan J;
PI   Paoni NF,  Roy MA,  Stewart TA,  Tumas D,  Watanabe CK,  Williams PM;
PI   Wood WI,  Zhang Z;
XX
DR   WPI; 2003-328482/31.
DR   P-PSDB; ABU72061.
XX
PT   Novel secreted and transmembrane polypeptide for modulating biological
PT   activity of cell expressing the polypeptide, for identifying agonists
PT   or antagonists of polypeptide, and as molecular weight markers -
XX
PS   Claim 2; Fig 51; 254pp; English.
XX
CC   The invention describes an isolated, secreted and transmembrane
CC   polypeptide (PP), termed PRO PP or fibroblast growth factor receptor PP
CC   (I). (I) is useful for detecting PRO533, PRO301, PRO187, PRO337,
CC   PRO1411, PRO10096, PRO246, PRO6307, PRO6003, fibroblast growth factor
CC   receptor (FGFR)-3, FGFR-4, FGFR-1, FGFR-2, PRO6004, PRO4356, PRO2630,
CC   PRO265 or PRO951 polypeptide, and for linking a bioactive molecule to a
CC   cell expressing the above polypeptides. The bioactive molecule, a toxin,
CC   radiolabel or an antibody, causes cell death. PRO is useful in assays to
CC   identify other proteins or molecules involved in binding interaction.
CC   The polynucleotide (II) encoding (I) is useful in chromosome and gene
CC   mapping, in generation of antisense RNA and DNA, for generating
CC   transgenic animals or knockout animals which in turn are useful in the
CC   development and screening of therapeutically useful reagents, to
CC   construct hybridisation probes for mapping the gene which encodes the
CC   PRO and for the genetic analysis of individuals with genetic disorders,
CC   in gene therapy, for chromosome identification and as a chromosome
CC   marker. (I) and (II) are useful for tissue typing. This sequence
CC   encodes a novel human secreted and transmembrane PRO polypeptide.
XX
SQ   Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

Alignment Scores:
Pred. No.:              8.55e-167       Length:         1679
Score:                  1806.00         Matches:        344
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     25              Gaps:           0

US-10-017-084A-523 (1-344) x ACA60526 (1-1679)

Qy          1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 193

Qy         21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        194 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 253

Qy         41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
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Db        254 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 313

Qy         61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        314 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 373

Qy         81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
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Db        374 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 433

Qy        101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493

Qy        121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        494 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 553

Qy        141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613

Qy        161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673

Qy        181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy        201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy        221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853

Qy        241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        854 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 913

Qy        261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 973

Qy        281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

Qy        301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1093

Qy        321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1153

Qy        341 LeuLeuLysPhe 344
              ||||||||||||
Db       1154 CTTCTCAAATTT 1165

RESULT 10
ACA03790
ID   ACA03790 standard; cDNA; 1679 BP.
XX
AC   ACA03790;
XX
DT   23-MAY-2003  (first entry)
XX
DE   cDNA encoding human PRO polypeptide #188.
XX
KW   Human; PRO polypeptide; secreted and transmembrane protein;
KW   tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
KW   differentiation; chondrocyte; tumour; genetic disorder;
KW   cytostatic; gene; ss.
XX
OS   Homo sapiens.
XX
PN   US2003036180-A1.
XX
PD   20-FEB-2003.
XX
PF   09-MAY-2002; 2002US-0143114.
XX
PR   31-MAR-1997;   97WO-US05230.
PR   12-JUN-1998;   98WO-US12456.
PR   14-JUL-1998;   98WO-US14552.
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PR 28-AUG-1998; 98WO-US17888.
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19093.
PR 14-SEP-1998; 98WO-US19094.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 29-OCT-1998; 98WO-US22991.
PR 29-OCT-1998; 98WO-US22992.
PR 20-NOV-1998; 98WO-US24855.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US05190.
PR 20-APR-1999; 99WO-US08615.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 22-DEC-1999; 99WO-US30720.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05746.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 20-DEC-2000; 2000US-0747259.
PR 28-FEB-2001; 2001US-0796498.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 18-MAY-2001; 2001US-0860216.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 21-JUN-2001; 2001US-0887879.
PR 18-JUL-2001; 2001US-0908827.
PR 06-AUG-2001; 2001US-0924419.
PR 09-AUG-2001; 2001US-0927796.
PR 16-AUG-2001; 2001US-0931836.
PR 19-DEC-2001; 2001US-0028072.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-332040/31.
DR P-PSDB; ABU66757.
XX
PT New secreted and transmembrane PRO nucleic acids, useful for gene
PT therapy, in chromosome and gene mapping, as chromosome markers, in
PT tissue typing, and in chromosome identification
XX
PS Claim 2; Fig 375; 660pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The
CC PRO polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for
CC linking bioactive molecules to cells expressing PRO polypeptides,
CC for modulating biological activities of cells expressing PRO
CC polypeptides, and for for identifying agonists or antagonists.
CC The PRO polypeptides are useful for for stimulating the release of
CC tumour necrosis factor (TNF)-alpha from human blood, for stimulating
CC the proliferation or differentiation of chondrocytes, and detecting the
CC presence of tumours. The polynucleotide sequences encoding PRO
CC polypeptides are useful as hybridisation probes, in chromosome and
CC gene mapping, in the generation of antisense RNA and DNA, in the
CC preparation of PRO polypeptides, for generating transgenic animals or
CC knockout animals, for the genetic analysis of individuals with genetic
CC disorders, and in gene therapy. ACA03603-ACA03877 represent cDNAs
CC encoding the human PRO polypeptides of the invention.
CC Note: The sequence data for this patent was obtained in electronic
CC format directly from the USPTO web site at
CC seqdata.uspto.gov/psipsDIDEntry.html.
XX
SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

Alignment Scores:

Pred. No.:	8.55e-167	Length:	1679
Score:	1806.00	Matches:	344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	25	Gaps:	0

US-10-017-084A-523 (1-344) x ACA03790 (1-1679)

Qy 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 193

Qy         21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys  40
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        194 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 253

Qy         41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp  60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        254 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 313

Qy         61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp  80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        314 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 373

Qy         81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 433

Qy        101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493

Qy        121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
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Db        494 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 553

Qy        141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613

Qy        161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
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Db        614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673

Qy        181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
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Db        674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy        201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy        221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
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Db        794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853

Qy        241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        854 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 913

Qy        261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 973

Qy        281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

Qy        301 LeuGlyHisThrAsnAlaSerIleMetLeuProGlyProGlyAlaValSerGluValSer 320
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Db       1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1093

Qy        321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1153

Qy        341 LeuLeuLysPhe 344
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Db       1154 CTTCTCAAATTT 1165

RESULT 11
ACA04211
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ID   ACA04211 standard; cDNA; 1679 BP.
XX
AC   ACA04211;
XX
DT   27-MAY-2003  (first entry)
XX
DE   Human cDNA encoding a secreted/transmembrane protein, SEQ ID 375.
XX
KW   Human; ss; gene; secreted protein; transmembrane protein; PRO;
KW   inflammatory disease; organ failure; atherosclerosis; cardiac injury;
KW   infertility; birth defects; premature aging; AIDS; biosensor;
KW   acquired immunodeficiency syndrome; cancer; diabetic complication;
KW   bioreactor; tumour.
XX
OS   Homo sapiens.
XX
PN   US2003032155-A1.
XX
PD   13-FEB-2003.
XX
PF   03-MAY-2002; 2002US-0137865.
XX
PR   31-MAR-1997;    97WO-US05230.
PR   12-JUN-1998;    98WO-US12456.
PR   14-JUL-1998;    98WO-US14552.
PR   28-AUG-1998;    98WO-US17888.
PR   10-SEP-1998;    98WO-US18824.
PR   14-SEP-1998;    98WO-US19093.
PR   14-SEP-1998;    98WO-US19094.
PR   14-SEP-1998;    98WO-US19177.
PR   16-SEP-1998;    98WO-US19330.
PR   17-SEP-1998;    98WO-US19437.
PR   07-OCT-1998;    98WO-US21141.
PR   29-OCT-1998;    98WO-US22991.
PR   29-OCT-1998;    98WO-US22992.
PR   20-NOV-1998;    98WO-US24855.
PR   01-DEC-1998;    98WO-US25108.
PR   05-JAN-1999;    99WO-US00106.
PR   08-MAR-1999;    99WO-US05028.
PR   10-MAR-1999;    99WO-US05190.
PR   20-APR-1999;    99WO-US08615.
PR   14-MAY-1999;    99WO-US10733.
PR   02-JUN-1999;    99WO-US12252.
PR   01-SEP-1999;    99WO-US20111.
PR   08-SEP-1999;    99WO-US20594.
PR   13-SEP-1999;    99WO-US20944.
PR   15-SEP-1999;    99WO-US21090.
PR   15-SEP-1999;    99WO-US21547.
PR   05-OCT-1999;    99WO-US23089.
PR   29-NOV-1999;    99WO-US28214.
PR   30-NOV-1999;    99WO-US28313.
PR   30-NOV-1999;    99WO-US28409.
PR   01-DEC-1999;    99WO-US28301.
PR   01-DEC-1999;    99WO-US28634.
PR   02-DEC-1999;    99WO-US28551.
PR   02-DEC-1999;    99WO-US28564.
PR   02-DEC-1999;    99WO-US28565.
PR   16-DEC-1999;    99WO-US30095.
PR   20-DEC-1999;    99WO-US30911.
PR   20-DEC-1999;    99WO-US30999.
PR   22-DEC-1999;    99WO-US30720.
PR   30-DEC-1999;    99WO-US31243.
PR   30-DEC-1999;    99WO-US31274.
PR   05-JAN-2000;  2000WO-US00219.
PR   06-JAN-2000;  2000WO-US00277.
PR   06-JAN-2000;  2000WO-US00376.
PR   11-FEB-2000;  2000WO-US03565.
PR   18-FEB-2000;  2000WO-US04341.
PR   18-FEB-2000;  2000WO-US04342.
PR   22-FEB-2000;  2000WO-US04414.
PR   24-FEB-2000;  2000WO-US04914.
PR   24-FEB-2000;  2000WO-US05004.
PR   01-MAR-2000;  2000WO-US05601.
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PR   02-MAR-2000; 2000WO-US05746.
PR   02-MAR-2000; 2000WO-US05841.
PR   10-MAR-2000; 2000WO-US06319.
PR   15-MAR-2000; 2000WO-US06884.
PR   20-MAR-2000; 2000WO-US07377.
PR   21-MAR-2000; 2000WO-US07532.
PR   30-MAR-2000; 2000WO-US08439.
PR   17-MAY-2000; 2000WO-US13705.
PR   22-MAY-2000; 2000WO-US14042.
PR   30-MAY-2000; 2000WO-US14941.
PR   02-JUN-2000; 2000WO-US15264.
PR   28-JUL-2000; 2000WO-US20710.
PR   11-AUG-2000; 2000WO-US22031.
PR   23-AUG-2000; 2000WO-US23522.
PR   24-AUG-2000; 2000WO-US23328.
PR   08-NOV-2000; 2000WO-US30952.
PR   10-NOV-2000; 2000WO-US30873.
PR   01-DEC-2000; 2000WO-US32678.
PR   20-DEC-2000; 2000WO-US34956.
PR   28-FEB-2001; 2001WO-US06520.
PR   01-MAR-2001; 2001WO-US06666.
PR   25-MAY-2001; 2001WO-US17092.
PR   01-JUN-2001; 2001WO-US17800.
PR   20-JUN-2001; 2001WO-US19692.
PR   22-JUN-2001; 2001WO-US20116.
PR   29-JUN-2001; 2001WO-US21066.
PR   09-JUL-2001; 2001WO-US21735.
PR   20-DEC-2000; 2000US-0747259.
PR   28-FEB-2001; 2001US-0796498.
PR   09-MAR-2001; 2001US-0802706.
PR   14-MAR-2001; 2001US-0808689.
PR   22-MAR-2001; 2001US-0816744.
PR   05-APR-2001; 2001US-0828366.
PR   10-MAY-2001; 2001US-0854208.
PR   10-MAY-2001; 2001US-0854280.
PR   18-MAY-2001; 2001US-0860216.
PR   25-MAY-2001; 2001US-0866028.
PR   25-MAY-2001; 2001US-0866034.
PR   01-JUN-2001; 2001US-0872035.
PR   05-JUN-2001; 2001US-0874503.
PR   14-JUN-2001; 2001US-0882636.
PR   19-JUN-2001; 2001US-0886342.
PR   21-JUN-2001; 2001US-0887879.
PR   18-JUL-2001; 2001US-0908827.
PR   06-AUG-2001; 2001US-0924419.
PR   09-AUG-2001; 2001US-0927796.
PR   16-AUG-2001; 2001US-0931836.
PR   19-DEC-2001; 2001US-0028072.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
PI   Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI   Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR   WPI; 2003-331925/31.
DR   P-PSDB; ABU67033.
XX
PT   New secreted and transmembrane nucleic acids and polypeptides,
PT   designated as PRO, useful for treating inflammation, organ failure,
PT   atherosclerosis, cardiac injury, infertility, birth defects, premature
PT   aging, AIDS, or cancer
XX
PS   Claim 2; Fig 375; 659pp; English.
XX
CC   The invention relates to an isolated nucleic acid comprising, or which is
CC   at least 80% identical to, or the full-length coding sequence of, any of
CC   the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
CC   (one of 275 secreted or transmembrane proteins). The nucleic acid
CC   further comprises the full-length coding sequence of the DNA deposited
CC   under American Type Culture Collection (ATCC) accession number in a list
CC   given in the specification. Also included are vectors and host
CC   cells for producing PRO proteins, PRO fusion proteins, anti-PRO
CC   antibodies, PRO extracellular domains and mature sequences, methods
CC   of detecting PRO proteins, methods for stimulating the release of
CC   TNF-alpha (tumour necrosis factor alpha) from human blood,
CC   (and the proliferation of differentiation of chondrocyte cells, the
CC   proliferation of, or gene expression in pericyte cells, the release or
CC   proteoglycans from cartilage, proliferation of inner ear urticular
CC   supporting cells, the proliferation of T-lymphocyte cells, the release
CC   of a cytokine from peripheral blood mononuclear cells (PBMC), or the
CC   proliferation of endothelial cells), a method for modulating the uptake
CC   of glucose or free fatty acid (FFA) by skeletal muscle cells,
CC   a method for inhibiting the binding of A-peptide to factor VIIA,
CC   or the differentiation of adipocyte cells, a method for detecting the
CC   presence of a tumour in a mammal and an oligonucleotide probe derived
CC   from any of the nucleotide sequences cited above. The nucleic acids and
CC   polypeptides are useful for treating inflammatory diseases, organ
CC   failure, atherosclerosis, cardiac injury, infertility, birth defects,
CC   premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or
CC   diabetic complications. The nucleic acids are useful as hybridisation
CC   probes, in chromosome and gene mapping, and in generating antisense RNA
CC   or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
CC   biosensors or bioreactors. Both are useful in tissue typing.
CC   The present sequence encodes a PRO protein of the invention.
XX
SQ   Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

Alignment Scores:
Pred. No.:                  8.55e-167       Length:          1679
Score:                      1806.00         Matches:         344
Percent Similarity:         100.00%         Conservative:    0
Best Local Similarity:      100.00%         Mismatches:      0
Query Match:                100.00%         Indels:          0
DB:                         25              Gaps:            0

US-10-017-084A-523 (1-344) x ACA04211 (1-1679)

Qy          1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 193

Qy         21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        194 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 253

Qy         41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        254 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 313

Qy         61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        314 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 373

Qy         81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 433

Qy        101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493

Qy        121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        494 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 553

Qy        141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613

Qy        161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673

Qy        181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
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Db        674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy        201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy        221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853

Qy        241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        854 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 913

Qy        261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
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Db        914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 973

Qy        281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

Qy        301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1093

Qy        321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
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Db       1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1153

Qy        341 LeuLeuLysPhe 344
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Db       1154 CTTCTCAAATTT 1165
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RESULT 12
ACA04516
ID ACA04516 standard; cDNA; 1679 BP.
XX
AC ACA04516;
XX
DT 28-MAY-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO337 DNA.
XX
KW Secreted and transmembrane polypeptide; PRO polypeptide; PRO533;
KW PRO301; PRO187; PRO337; PRO1411; PRO10096; PRO246; PRO6307; PRO6003;
KW PRO6004; PRO4356; PRO2630; PRO265; PRO941; FGFR; bioactive molecule;
KW fibroblast growth factor receptor; cell death; chromosome mapping;
KW gene mapping; transgenic animal; knockout animal; gene therapy;
KW tumour; obesity; diabetes; insulinaemia; vascular permeability;
KW cardiac insufficiency disorder; immune response; hearing loss;
KW auditory hair cell regeneration; bone disorder; cartilage disorder;
KW sports injury; arthritis; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003032062-A1.
XX
PD 13-FEB-2003.
XX
PF 01-FEB-2002; 2002US-0066273.
XX
PR 14-JUL-1998; 98WO-US14552.
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19093.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 20-NOV-1998; 98WO-US24855.
PR 25-NOV-1998; 98WO-US25190.
PR 01-DEC-1998; 98WO-US25108.
PR 08-MAR-1999; 99WO-US05028.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28565.
PR 20-DEC-1999; 99WO-US30999.
PR 05-JAN-2000; 2000WO-US00219.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 09-MAR-2000; 2000WO-US06471.
PR 20-MAR-2000; 2000WO-US07377.
PR 30-MAR-2000; 2000WO-US08439.
PR 15-MAY-2000; 2000WO-US13358.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 01-DEC-2000; 2000WO-US32678.
PR 28-FEB-2001; 2001WO-US06520.
PR 30-MAY-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 26-AUG-1997; 97US-056974P.
PR 17-SEP-1997; 97US-059115P.
PR 18-SEP-1997; 97US-059263P.
PR 19-SEP-1997; 97US-059588P.
PR 17-OCT-1997; 97US-062285P.
PR 24-OCT-1997; 97US-062816P.
PR 24-OCT-1997; 97US-063082P.
PR 27-OCT-1997; 97US-063329P.
PR 29-OCT-1997; 97US-063733P.
PR 21-NOV-1997; 97US-066364P.
PR 25-NOV-1997; 97US-066840P.
PR 16-DEC-1997; 97US-069694P.
PR 09-FEB-1998; 98US-074086P.
PR 09-FEB-1998; 98US-074092P.
PR 25-MAR-1998; 98US-079294P.
PR 08-APR-1998; 98US-081049P.
PR 10-AUG-1998; 98US-095998P.
PR 18-AUG-1998; 98US-097000P.
PR 09-SEP-1998; 98US-099601P.
PR 10-SEP-1998; 98US-099803P.
PR 10-SEP-1998; 98US-099811P.
PR 10-SEP-1998; 98US-099812P.
PR 17-SEP-1998; 98US-100858P.
PR 24-SEP-1998; 98US-101922P.
PR 28-OCT-1998; 98US-106032P.
PR 20-NOV-1998; 98US-109304P.
PR 23-MAR-1999; 99US-125778P.
PR 15-JUN-1999; 99US-139695P.
PR 20-JUL-1999; 99US-145070P.
PR 26-JUL-1999; 99US-145698P.
PR 17-AUG-1999; 99US-149396P.
PR 07-DEC-1999; 99US-169495P.
PR 15-NOV-2001; 2001US-0002796.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;
XX

DR WPI; 2003-341963/32.
DR P-PSDB; ABU67162.
XX
PT New secreted and transmembrane polypeptide for modulating biological
PT activity of a cell expressing the polypeptide, identifying agonists or
PT antagonists of the polypeptide, and as molecular weight markers
XX
PS Claim 2; Fig 51; 254pp; English.
XX
CC The invention describes an isolated, secreted and transmembrane
CC polypeptide (I), termed PRO polypeptide. (I) Is useful for detecting
CC PRO533, PRO301, PRO187, PRO337, PRO1411, PRO10096, PRO246, PRO6307,
CC PRO6003, PRO6004, PRO4356, PRO2630, PRO265, PRO941, fibroblast growth
CC factor receptor (FGFR)-4, FGFR-3, FGFR-2 or FGFR-1 polypeptide, and for
CC linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a
CC cell expressing the polypeptides. The bioactive molecule causes cell
CC death. (II) Is useful as hybridisation probes, in chromosome and gene
CC mapping, in generation of antisense RNA and DNA, in the preparation of
CC PRO polypeptide, for generating transgenic animals or knockout animals
CC which in turn are useful in the development and screening of
CC therapeutically useful reagents, and for the genetic analysis of
CC individuals with genetic disorders, in gene therapy, and for chromosome
CC identification. (I) Or Ab is useful for the preparation of medicament for
CC treating conditions which are responsive to the PRO polypeptide or
CC anti-PRO antibody e.g. a tumour. (I) is useful for treating obesity,
CC diabetes or hypo- or hyper-insulinaemia, and cardiac insufficiency
CC disorders, for inhibiting tumour growth, enhances vascular permeability
CC and immune response, for inducing regeneration of auditory hair cells and
CC for treating hearing loss in mammals, and for treating bone and/or
CC cartilage disorders such as sports injuries and arthritis. This sequence
CC encodes a novel human secreted and transmembrane polypeptide.
XX
SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

Alignment Scores:

Pred. No.:	8.55e-167	Length:	1679
Score:	1806.00	Matches:	344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	25	Gaps:	0

US-10-017-084A-523 (1-344) x ACA04516 (1-1679)

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Qy        1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
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Db      134 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 193

Qy       21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
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Db      194 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 253

Qy       41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
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Db      254 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 313

Qy       61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
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Db      314 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 373

Qy       81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
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Db      374 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 433

Qy      101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
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Db      434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493

Qy      121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
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Qy      141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
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Db      554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613

Qy      161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
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Db      614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673

Qy      181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
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Db      674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy      201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
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Db      734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy      221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
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Db      794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853

Qy      241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      854 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 913

Qy      261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 973

Qy      281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

Qy      301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1093

Qy      321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
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Db     1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1153

Qy      341 LeuLeuLysPhe 344
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Db     1154 CTTCTCAAATTT 1165
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RESULT 13
ACA04996
ID ACA04996 standard; cDNA; 1679 BP.
XX
AC ACA04996;
XX
DT 28-MAY-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO337 cDNA.
XX
KW Secreted and transmembrane polypeptide; PRO polypeptide; PRO533;
KW PRO301; PRO187; PRO337; PRO1411; PRO10096; PRO246; PRO6307; PRO6003;
KW PRO6004; PRO4356; PRO2630; PRO265; PRO941; FGFR; bioactive molecule;
KW fibroblast growth factor receptor; cell death; chromosome mapping;
KW gene mapping; transgenic animal; knockout animal; gene therapy;
KW tumour; obesity; diabetes; insulinaemia; vascular permeability;
KW cardiac insufficiency disorder; immune response; hearing loss;
KW auditory hair cell regeneration; bone disorder; cartilage disorder;
KW sports injury; arthritis; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003032063-A1.
XX
PD 13-FEB-2003.
XX
PF 01-FEB-2002; 2002US-0066494.
XX
PR 14-SEP-1998; 98WO-US19093.
PR 16-SEP-1998; 98WO-US19330.

PR 17-SEP-1998; 98WO-US19437.
PR 20-NOV-1998; 98WO-US24855.
PR 25-NOV-1998; 98WO-US25190.
PR 01-DEC-1998; 98WO-US25108.
PR 08-MAR-1999; 99WO-US05028.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28565.
PR 20-DEC-1999; 99WO-US30999.
PR 05-JAN-2000; 2000WO-US00219.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 09-MAR-2000; 2000WO-US06471.
PR 20-MAR-2000; 2000WO-US07377.
PR 30-MAR-2000; 2000WO-US08439.
PR 15-MAY-2000; 2000WO-US13358.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 01-DEC-2000; 2000WO-US32678.
PR 28-FEB-2001; 2001WO-US06520.
PR 30-MAY-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 26-AUG-1997; 97US-056974P.
PR 17-SEP-1997; 97US-059115P.
PR 18-SEP-1997; 97US-059263P.
PR 19-SEP-1997; 97US-059588P.
PR 17-OCT-1997; 97US-062285P.
PR 24-OCT-1997; 97US-062816P.
PR 24-OCT-1997; 97US-063082P.
PR 27-OCT-1997; 97US-063329P.
PR 29-OCT-1997; 97US-063733P.
PR 21-NOV-1997; 97US-066364P.
PR 25-NOV-1997; 97US-066840P.
PR 16-DEC-1997; 97US-069694P.
PR 09-FEB-1998; 98US-074086P.
PR 09-FEB-1998; 98US-074092P.
PR 25-MAR-1998; 98US-079294P.
PR 08-APR-1998; 98US-081049P.
PR 10-AUG-1998; 98US-095998P.
PR 18-AUG-1998; 98US-097000P.
PR 09-SEP-1998; 98US-099601P.
PR 10-SEP-1998; 98US-099803P.
PR 10-SEP-1998; 98US-099811P.
PR 10-SEP-1998; 98US-099812P.
PR 17-SEP-1998; 98US-100858P.
PR 24-SEP-1998; 98US-101922P.
PR 28-OCT-1998; 98US-106032P.
PR 20-NOV-1998; 98US-109304P.
PR 23-MAR-1999; 99US-125778P.
PR 15-JUN-1999; 99US-139695P.
PR 20-JUL-1999; 99US-145070P.
PR 26-JUL-1999; 99US-145698P.
PR 17-AUG-1999; 99US-149396P.
PR 07-DEC-1999; 99US-169495P.
PR 15-NOV-2001; 2001US-0002796.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;
XX
DR WPI; 2003-341964/32.
DR P-PSDB; ABU67293.
XX
PT Thirty seven nucleic acids encoding novel secreted and transmembrane
PT PRO polypeptides, useful for modulating biological activity of cell
PT expressing the polypeptide, and in chromosome and gene mapping -
XX
PS Claim 2; Fig 51; 255pp; English.
XX
CC The invention describes an isolated, secreted and transmembrane
CC polypeptide (I), termed PRO polypeptide. (I) Is useful for detecting
CC PRO533, PRO301, PRO187, PRO337, PRO1411, PRO10096, PRO246, PRO6307,
CC PRO6003, PRO6004, PRO4356, PRO2630, PRO265, PRO941, fibroblast growth
CC factor receptor (FGFR)-4, FGFR-3, FGFR-2 or FGFR-1 polypeptide, and for
CC linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a
CC cell expressing the polypeptides. The bioactive molecule causes cell
CC death. (II) Is useful as hybridisation probes, in chromosome and gene
CC mapping, in generation of antisense RNA and DNA, in the preparation of
CC PRO polypeptide, for generating transgenic animals or knockout animals
CC which in turn are useful in the development and screening of
CC therapeutically useful reagents, and for the genetic analysis of
CC individuals with genetic disorders, in gene therapy, and for chromosome
CC identification. (I) Or Ab is useful for the preparation of medicament for
CC treating conditions which are responsive to the PRO polypeptide or
CC anti-PRO antibody e.g. a tumour. (I) is useful for treating obesity,
CC diabetes or hypo- or hyper-insulinaemia, and cardiac insufficiency
CC disorders, for inhibiting tumour growth, enhances vascular permeability
CC and immune response, for inducing regeneration of auditory hair cells and
CC for treating hearing loss in mammals, and for treating bone and/or
CC cartilage disorders such as sports injuries and arthritis. This sequence
CC encodes a novel human secreted and transmembrane polypeptide
CC associated oligonucleotide.
XX
SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

Alignment Scores:

Pred. No.:	8.55e-167	Length:	1679
Score:	1806.00	Matches:	344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	25	Gaps:	0

US-10-017-084A-523 (1-344) x ACA04996 (1-1679)

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Qy          1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
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Db        134 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 193

Qy         21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
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Db        194 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 253

Qy         41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
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Db        254 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 313

Qy         61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
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Db        314 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 373

Qy         81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
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Qy        101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
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Db        434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493

Qy        121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
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Db        494 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 553

Qy        141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
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Db        554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613

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Db        614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673

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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy        201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy        221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853

Qy        241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        854 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 913

Qy        261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
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Db        914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 973

Qy        281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
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Db        974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

Qy        301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
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Db       1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1093

Qy        321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
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Db       1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1153

Qy        341 LeuLeuLysPhe 344
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Db       1154 CTTCTCAAATTT 1165

RESULT 14
ABX89328
ID   ABX89328 standard; cDNA; 1679 BP.
XX
AC   ABX89328;
XX
DT   13-MAY-2003  (first entry)
XX
DE   DNA encoding novel secreted and transmembrane protein PRO337.
XX
KW   Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW   cardiac insufficiency disorder; cancer; tumour; immune response;
KW   adrenal cortical capillary endothelial growth; c-fos induction;
KW   vascular endothelial growth factor inhibition; VEGF inhibition;
KW   endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW   retinal neurons cell survival; rod photoreceptor cell survival;
KW   retinal disorder; retinitis pigmentosum; kidney disorder;
KW   mammalian kidney mesangial cell proliferation; Berger disease;
KW   dermatitis; herpetiformis; Crohn's disease; chondrocyte proliferation;
KW   chondrocyte redifferentiation; sports injury; arthritis; gene; ss.
XX
OS   Homo sapiens.
XX
PN   US2003017563-A1.
XX
PD   23-JAN-2003.
XX
PF   07-MAY-2002; 2002US-0140808.
XX
PR   31-MAR-1997;   97WO-US05230.
PR   12-JUN-1998;   98WO-US12456.
PR   14-JUL-1998;   98WO-US14552.
PR   28-AUG-1998;   98WO-US17888.
PR   10-SEP-1998;   98WO-US18824.
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PR   14-SEP-1998;   98WO-US19094.
PR   14-SEP-1998;   98WO-US19177.
PR   16-SEP-1998;   98WO-US19330.
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PR   07-OCT-1998;   98WO-US21141.
PR   29-OCT-1998;   98WO-US22991.
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PR   08-MAR-1999;   99WO-US05028.
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PR   20-APR-1999;   99WO-US08615.
PR   14-MAY-1999;   99WO-US10733.
PR   02-JUN-1999;   99WO-US12252.
PR   01-SEP-1999;   99WO-US20111.
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PR   01-DEC-1999;   99WO-US28634.
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PR   02-DEC-1999;   99WO-US28565.
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PR   30-DEC-1999;   99WO-US31274.
PR   05-JAN-2000; 2000WO-US00219.
PR   06-JAN-2000; 2000WO-US00277.
PR   06-JAN-2000; 2000WO-US00376.
PR   11-FEB-2000; 2000WO-US03565.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   22-FEB-2000; 2000WO-US04414.
PR   24-FEB-2000; 2000WO-US04914.
PR   24-FEB-2000; 2000WO-US05004.
PR   01-MAR-2000; 2000WO-US05601.
PR   02-MAR-2000; 2000WO-US05746.
PR   02-MAR-2000; 2000WO-US05841.
PR   10-MAR-2000; 2000WO-US06319.
PR   15-MAR-2000; 2000WO-US06884.
PR   20-MAR-2000; 2000WO-US07377.
PR   21-MAR-2000; 2000WO-US07532.
PR   30-MAR-2000; 2000WO-US08439.
PR   17-MAY-2000; 2000WO-US13705.
PR   22-MAY-2000; 2000WO-US14042.
PR   30-MAY-2000; 2000WO-US14941.
PR   02-JUN-2000; 2000WO-US15264.
PR   28-JUL-2000; 2000WO-US20710.
PR   11-AUG-2000; 2000WO-US22031.
PR   23-AUG-2000; 2000WO-US23522.
PR   24-AUG-2000; 2000WO-US23328.
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PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 20-DEC-2000; 2000US-0747259.
PR 28-FEB-2001; 2001US-0796498.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 18-MAY-2001; 2001US-0860216.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 21-JUN-2001; 2001US-0887879.
PR 18-JUL-2001; 2001US-0908827.
PR 06-AUG-2001; 2001US-0924419.
PR 09-AUG-2001; 2001US-0927796.
PR 16-AUG-2001; 2001US-0931836.
PR 19-DEC-2001; 2001US-0028072.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-148238/14.
DR P-PSDB; ABU59838.
XX
PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT are therapeutically useful for enhancing immune response and in cancer
PT treatments
XX
PS Claim 2; Fig 375; 659pp; English.
XX
CC The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813
CC and PRO11066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpetiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and
CC are thus useful for treating sports injuries, and arthritis. This
CC sequence encodes a novel human PRO protein.
XX
SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

Alignment Scores:

Pred. No.:	8.55e-167	Length:	1679
Score:	1806.00	Matches:	344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	25	Gaps:	0

US-10-017-084A-523 (1-344) x ABX89328 (1-1679)

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Qy          1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
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Db        134 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 193

Qy         21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
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Db        194 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 253

Qy         41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
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Db        254 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 313

Qy         61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        314 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 373

Qy         81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
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Db        374 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 433

Qy        101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
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Qy        121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
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Qy        141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
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Qy        161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
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Db        614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673

Qy        181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
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Db        674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy        201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
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Db        734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy        221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
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Db        794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853

Qy        241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
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Db        854 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 913

Qy        261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
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Db        914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 973

Qy        281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
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Db        974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

Qy        301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
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Qy        321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
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Qy        341 LeuLeuLysPhe 344
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Db       1154 CTTCTCAAATTT 1165

RESULT 15
ABX92696
ID   ABX92696 standard; cDNA; 1679 BP.
XX
AC   ABX92696;
XX
DT   08-MAY-2003  (first entry)
XX
DE   cDNA encoding human PRO337 polypeptide.
XX
KW   Human; PRO polypeptide; secreted and transmembrane protein;
KW   immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;
KW   cardiac insufficiency; nervous system disorder; kidney disorder;
KW   bone disorder; cartilage disorder; arthritis; tumour; wound healing;
KW   genetic disorder; cytostatic; antidiabetic; antiinflammatory;
KW   antiarthritic; anti-tumour; vulnerary; antianaemic; dermatological;
KW   cardiant; gene; ss.
XX
OS   Homo sapiens.
XX
PN   US2002169284-A1.
XX
PD   14-NOV-2002.
XX
PF   16-OCT-2001; 2001US-0978697.
XX
PR   07-OCT-1998;   98WO-US21141.
PR   20-NOV-1998;   98WO-US24855.
PR   05-JAN-1999;   99WO-US00106.
PR   08-MAR-1999;   99WO-US05028.
PR   10-MAR-1999;   99WO-US05190.
PR   14-MAY-1999;   99WO-US10733.
PR   02-JUN-1999;   99WO-US12252.
PR   30-NOV-1999;   99WO-US28313.
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PR   09-JUL-2001; 2001WO-US21735.
PR   17-OCT-1997;   97US-062250P.
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PR   26-MAY-1981;   81US-0267213.
PR   17-MAR-1998;   98US-0040220.
PR   26-JUN-1998;   98US-0105413.
PR   07-OCT-1998;   98US-0168978.
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PR   06-NOV-1998;   98US-0187368.
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PR   22-DEC-1998;   98US-0218517.
PR   05-MAR-1999;   99US-0254465.
PR   10-MAR-1999;   99US-0265686.
PR   12-APR-1999;   99US-0284291.
PR   14-MAY-1999;   99US-0311832.
PR   14-MAY-1999;   99US-0380137.
PR   25-AUG-1999;   99US-0380138.
PR   25-AUG-1999;   99US-0380142.
PR   08-NOV-2000; 2000US-0709238.
PR   27-NOV-2000; 2000US-0723749.
PR   20-DEC-2000; 2000US-0747259.
PR   22-MAR-2001; 2001US-0816744.
PR   22-MAR-2001; 2001US-0816920.
PR   10-MAY-2001; 2001US-0854208.
PR   10-MAY-2001; 2001US-0854280.
PR   01-JUN-2001; 2001US-0872035.
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PR   19-JUN-2001; 2001US-0886342.
PR   30-JUL-2001; 2001US-0918585.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi A,  Baker KP,  Botstein D,  Desnoyers L,  Eaton D;
PI   Ferrara N,  Filvaroff E,  Fong S,  Gao W,  Gerber H,  Gerritsen ME;
PI   Goddard A,  Godowski PJ,  Grimaldi JC,  Gurney AL,  Hillan KJ;
PI   Kljavin IJ,  Kuo SS,  Napier MA,  Pan J,  Paoni NF,  Roy MA;
PI   Shelton DL,  Stewart TA,  Tumas D,  Williams PM,  Wood WI;
XX
DR   WPI; 2003-288163/28.
DR   P-PSDB; ABU61159.
XX
PT   Novel secreted and transmembrane polypeptides and polynucleotides
PT   encoding them useful for treating cancer, kidney diseases, bone,
```

PT cartilage disorders and immune deficiencies -
XX
PS Claim 2; Fig 221; 459pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The
CC PRO polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for
CC linking bioactive molecules to cells expressing PRO polypeptides,
CC for modulating biological activities of cells expressing PRO
CC polypeptides, and for for identifying agonists or antagonists. The
CC bioactive molecule maybe a toxin, radiolabel or antibody, and causes
CC apoptosis or death of the cell. The PRO polypeptides are useful for
CC treating immune disorders, diabetes or hyper- or hypo-insulinaemia,
CC cardiac insufficiency, nervous system disorders, kidney disorders,
CC bone and cartilage disorders or arthritis, tumours, and wound healing.
CC The polynucleotide sequences encoding PRO polypeptides are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, in the preparation of PRO polypeptides, for
CC generating transgenic animals or knockout animals, for the genetic
CC analysis of individuals with genetic disorders, and in gene therapy.
CC The present sequence encodes a human PRO polypeptide of the invention.
CC Note: The sequence data for this patent was obtained in electronic
CC format directly from the USPTO web site at
CC seqdata.uspto.gov/psipsDIDEntry.html.
XX
SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 other;

Alignment Scores:

Pred. No.:	8.55e-167	Length:	1679
Score:	1806.00	Matches:	344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	25	Gaps:	0

US-10-017-084A-523 (1-344) x ABX92696 (1-1679)

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Qy          1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
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Db        134 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 193

Qy         21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        194 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 253

Qy         41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        254 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 313

Qy         61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        314 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 373

Qy         81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 433

Qy        101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
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Db        434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493

Qy        121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
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Db        494 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 553

Qy        141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
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Db        554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613

Qy        161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673

Qy        181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy        201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy        221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853

Qy        241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
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Qy        261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
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Db        914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 973

Qy        281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
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Db        974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

Qy        301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1093

Qy        321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1153

Qy        341 LeuLeuLysPhe 344
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Db       1154 CTTCTCAAATTT 1165
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Search completed: September 11, 2003, 03:13:59
Job time : 379 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 11, 2003, 03:14:04 ; Search time 93 Seconds
(without alignments)
1632.643 Million cell updates/sec

Title: US-10-017-084A-523
Perfect score: 1806
Sequence: 1 MKTIQPKMHNSISWAIFTGL.....RRAGCVWLLPLLVLHLLLKF 344

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10017084/runat_09092003_141327_21903/app_query.fasta_1.519
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	926.5	51.3	1014	2	US-08-414-657D-5	Sequence 5, Appli
2	926.5	51.3	1014	4	US-09-135-080-7	Sequence 7, Appli
3	926.5	51.3	1238	2	US-08-414-657D-3	Sequence 3, Appli
4	926.5	51.3	1238	4	US-09-135-080-3	Sequence 3, Appli
5	923.5	51.1	977	2	US-08-414-657D-1	Sequence 1, Appli
6	923.5	51.1	977	4	US-09-135-080-1	Sequence 1, Appli
7	908	50.3	924	2	US-08-414-657D-7	Sequence 7, Appli
8	907	50.2	945	2	US-08-414-657D-8	Sequence 8, Appli
9	902	49.9	912	2	US-08-414-657D-6	Sequence 6, Appli
10	886.5	49.1	861	2	US-08-414-657D-9	Sequence 9, Appli
11	885.5	49.0	861	2	US-08-414-657D-10	Sequence 10, Appl
12	796.5	44.1	756	2	US-08-414-657D-17	Sequence 17, Appl
13	795.5	44.0	756	2	US-08-414-657D-18	Sequence 18, Appl
14	263.5	14.6	6814	4	US-09-484-970B-66	Sequence 66, Appl
15	256	14.2	1266	2	US-08-659-984A-2	Sequence 2, Appli
16	256	14.2	1266	3	US-08-660-531-2	Sequence 2, Appli
17	256	14.2	1335	2	US-08-659-984A-4	Sequence 4, Appli
18	256	14.2	1335	3	US-08-660-531-4	Sequence 4, Appli
19	246.5	13.6	3360	1	US-08-408-093-5	Sequence 5, Appli
20	246.5	13.6	3360	1	US-08-408-420A-5	Sequence 5, Appli
21	246.5	13.6	3360	1	US-08-714-901-5	Sequence 5, Appli
22	246.5	13.6	3360	3	US-08-040-741-5	Sequence 5, Appli
23	237	13.1	219	2	US-08-414-657D-11	Sequence 11, Appl
24	237	13.1	219	2	US-08-414-657D-12	Sequence 12, Appl
25	230.5	12.8	2869	1	US-08-374-834-2	Sequence 2, Appli
26	230.5	12.8	2869	1	US-08-644-271-2	Sequence 2, Appli
27	230.5	12.8	2869	4	US-09-077-955-2	Sequence 2, Appli
28	230	12.7	2610	1	US-08-374-834-17	Sequence 17, Appl
29	230	12.7	2610	1	US-08-644-271-28	Sequence 28, Appl
30	230	12.7	2610	4	US-09-077-955-32	Sequence 32, Appl
31	225.5	12.5	1581	5	PCT-US95-08493-14	Sequence 14, Appl
32	225.5	12.5	2580	5	PCT-US95-08493-18	Sequence 18, Appl
33	225.5	12.5	2604	5	PCT-US95-08493-20	Sequence 20, Appl
34	220.5	12.2	1598	4	US-09-778-510-19	Sequence 19, Appl
35	220.5	12.2	1935	4	US-09-778-510-21	Sequence 21, Appl
36	219	12.1	4843	3	US-08-986-485-1	Sequence 1, Appli
37	213.5	11.8	1718	4	US-09-778-510-5	Sequence 5, Appli
38	213	11.8	177	2	US-08-414-657D-13	Sequence 13, Appl
39	212	11.7	177	2	US-08-414-657D-14	Sequence 14, Appl
40	211	11.7	1273	4	US-09-778-510-3	Sequence 3, Appli
41	210	11.6	4078	4	US-09-016-434-1120	Sequence 1120, Ap
42	209	11.6	3402	4	US-09-996-243-118	Sequence 118, App
43	205.5	11.4	1542	4	US-09-205-258-123	Sequence 123, App
44	205	11.4	1820	4	US-09-778-510-1	Sequence 1, Appli
45	203.5	11.3	5824	4	US-09-620-312D-72	Sequence 72, Appl

ALIGNMENTS

RESULT 1
US-08-414-657D-5
; Sequence 5, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:

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;       TELEPHONE:  609-520-3214
;       TELEFAX:  609-520-3259
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1014 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     FEATURE:
;       NAME/KEY:  Coding Sequence
;       LOCATION:  1...1014
;       OTHER INFORMATION:
US-08-414-657D-5

Alignment Scores:
Pred. No.:              4.54e-99        Length:         1014
Score:                  926.50          Matches:        179
Percent Similarity:     73.54%          Conservative:   60
Best Local Similarity:  55.08%          Mismatches:     81
Query Match:            51.30%          Indels:         5
DB:                     2               Gaps:           4

US-10-017-084A-523 (1-344) x US-08-414-657D-5 (1-1014)

Qy         20 LeuAlaAlaLeuCysLeuPhe---GlnGlyValProValArgSerGlyAspAlaThrPhe 38
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Db         49 CTGAGACTGCTCTGCCTTCTTCCCACAGGACTGCCCGTTCGCAGCGTGGAT------TTT 102

Qy         39 ProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThr 58
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Db        103 AACCGAGGCACGGACAACATCACCGTGAGGCAGGGGGACACGGCCATCCTCAGGTGTGTG 162

Qy         59 IleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGly 78
              ::::::::::::   ::::::||||||||||||||||||||||   |||:::::|||||
Db        163 GTAGAAGACAAGAACTCGAAAGTGGCCTGGTTGAACCGCTCTGGCATCATCTTCGCTGGA 222

Qy         79 AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyr 98
              :::||||||||||   ||||||||||||||||   |||                :::|||
Db        223 CACGACAAGTGGTCTCTGGACCCTCGGGTTGAGCTGGAGAAACGCCATGCTCTGGAATAC 282

Qy         99 SerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGln 118
              !||:::   ||||||   ||||||||||||||||||||   ||||||||||||||||||
Db        283 AGCCTCCGAATCCAGAAGGTGGATGTCTATGATGAAGGATCCTACACATGCTCAGTTCAG 342

Qy        119 ThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle 138
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Db        343 ACACAGCATGAGCCCAAGACCTCTCAAGTTTACTTGATTGTACAAGTTCCACCAAAGATC 402

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Qy        159 AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly 178
              |||   ||||||||||||||   :::||||||||||||:::::::|||
Db        463 GCCAATGGGCGCCCTGAACCTGTTATCACCTGGAGACACCTTACACCACTTGGAAGAGAA 522

Qy        179 PheValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAsp 198
              |||      |||:::|||||||||||||||   ||||||||||||||||||||||
Db        523 TTTGAAGGAGAAGAAGAATATCTGGAGATCCTAGGCATCACCAGGGAACAGTCAGGCAAA 582

Qy        199 TyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThr 218
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Db        643 GTGAACTATCCACCCACCATCACAGAGTCTAAGAGCAATGAAGCCACCACAGGACGACAA 702

Qy        239 GlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAsp 258
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Qy        279 LysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSer 298
                 |||        ||||||:::|||      |||||||||||||||||||||||:::
Db        820 TCCCTGACGGTGACCAACGTCACTGAGGAACACTACGGCAACTATACCTGTGTGGCTGCC 879

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Db        880 AACAAGCTCGGCGTCACCAATGCCAGCCTAGTCCTTTTCAGACCCGGGTCGGTGAGAGGA 939

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Db        940 ATC---AACGGATCCATCAGTCTGGCCGTACCACTGTGGCTGCTGGCAGCGTCCCTGTTC 996

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RESULT 2
US-09-135-080-7
; Sequence 7, Application US/09135080
; Patent No. 6423827
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat R.
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/135,080
;      FILING DATE:  17-AUG-1998
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/414,657
;      FILING DATE:  31-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-620-3214
;      TELEFAX:  609-620-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1014 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...1014
;      OTHER INFORMATION:
US-09-135-080-7

Alignment Scores:
Pred. No.:              4.54e-99        Length:         1014
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Score:                 926.50        Matches:      179
Percent Similarity:    73.54%        Conservative:  60
Best Local Similarity: 55.08%        Mismatches:    81
Query Match:           51.30%        Indels:         5
DB:                    4             Gaps:           4

US-10-017-084A-523 (1-344) x US-09-135-080-7 (1-1014)

Qy         20 LeuAlaAlaLeuCysLeuPhe---GlnGlyValProValArgSerGlyAspAlaThrPhe 38
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Qy         39 ProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThr 58
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Db        103 AACCGAGGCACGGACAACATCACCGTGAGGCAGGGGGACACGGCCATCCTCAGGTGTGTG 162

Qy         59 IleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGly 78
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Db        163 GTAGAAGACAAGAACTCGAAAGTGGCCTGGTTGAACCGCTCTGGCATCATCTTCGCTGGA 222

Qy         79 AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyr 98
              :::||||||||||   ||||||||||||||   |||                  :::|||
Db        223 CACGACAAGTGGTCTCTGGACCCTCGGGTTGAGCTGGAGAAACGCCATGCTCTGGAATAC 282

Qy         99 SerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGln 118
              |||:::   ||||||   ||||||||||||||||||||   ||||||||||||||||||
Db        283 AGCCTCCGAATCCAGAAGGTGGATGTCTATGATGAAGGATCCTACACATGCTCAGTTCAG 342

Qy        119 ThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle 138
              |||   :::   ||||||||||||:::|||:::|||||||||||||||   |||||||||
Db        343 ACACAGCATGAGCCCAAGACCTCTCAAGTTTACTTGATTGTACAAGTTCCACCAAAGATC 402

Qy        139 ValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIle 158
              ||||||||||||:::::::::|||||||||:::|||:::::|||   |||:::
Db        403 TCCAACATCTCCTCGGATGTCACTGTGAATGAGGGCAGCAATGTAACCCTGGTCTGCATG 462

Qy        159 AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly 178
              |||   ||||||||||||||||   :::|||||||||||||:::::::|||
Db        463 GCCAATGGGCGCCCTGAACCTGTTATCACCTGGAGACACCTTACACCACTTGGAAGAGAA 522

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              |||      |||:::|||||||||||||   ||||||||||||||||||||||||
Db        523 TTTGAAGGAGAAGAAGAATATCTGGAGATCCTAGGCATCACCAGGGAACAGTCAGGCAAA 582

Qy        199 TyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThr 218
              |||||||||  |||:::|||:::|||::::::      |||:::::|||||||||||||
Db        583 TATGAGTGCAAGGCTGCCAACGAGGTCTCCTCCGCGGATGTCAAACAAGTCAAGGTCACT 642

Qy        219 ValAsnTyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLys 238
              ||||||||||||||   |||:::|||:::|||                  |||::::::
Db        643 GTGAACTATCCACCCACCATCACAGAGTCTAAGAGCAATGAAGCCACCACAGGACGACAA 702

Qy        239 GlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAsp 258
                 :::|||:::||||||||||||||||||||||:::   :::|||:::||||||:::|||
Db        703 GCTTCCCTCAAATGTGAAGCCTCAGCGGTGCCTGCACCTGACTTTGAGTGGTACCGGGAT 762

Qy        259 AspLysArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSer 278
              |||   |||   |||            |||:::::::::::::::            |||
Db        763 GACACCAGG---ATAAACAGTGCAAACGGCCTTGAGATTAAGAGCACTGAGGGCCAGTCC 819

Qy        279 LysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSer 298
                 |||      |||||||:::|||      ||||||||||||||||||||||||:::
Db        820 TCCCTGACGGTGACCAACGTCACTGAGGAACACTACGGCAACTATACCTGTGTGGCTGCC 879

Qy        299 AsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGlu 318
              ||||||||||||   ||||||||||:::::::|||||   ||||||:::|||
Db        880 AACAAGCTCGGCGTCACCAATGCCAGCCTAGTCCTTTTCAGACCCGGGTCGGTGAGAGGA 939

Qy        319 ValSerAsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeu 338
              :::   ||||||:::          |||      :::|||||||||          :::
Db        940 ATC---AACGGATCCATCAGTCTGGCCGTACCACTGTGGCTGCTGGCAGCGTCCCTGTTC 996

Qy        339 HisLeuLeuLeuLys 343
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                 ||||||  | |||
Db         997 TGCCTTCTCAGCAAA 1011

RESULT 3
US-08-414-657D-3
; Sequence 3, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1238 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  56...1069
;      OTHER INFORMATION:
US-08-414-657D-3

Alignment Scores:
Pred. No.:             6.2e-99       Length:        1238
Score:                 926.50        Matches:       179
Percent Similarity:    73.54%        Conservative:  60
Best Local Similarity: 55.08%        Mismatches:    81
Query Match:           51.30%        Indels:        5
DB:                    2             Gaps:          4

US-10-017-084A-523 (1-344) x US-08-414-657D-3 (1-1238)

Qy         20 LeuAlaAlaLeuCysLeuPhe---GlnGlyValProValArgSerGlyAspAlaThrPhe 38
              |||      |||||||||         |||:::|||||||||||||   |||      |||
Db        104 CTGAGACTGCTCTGCCTTCTTCCCACAGGACTGCCCGTTCGCAGCGTGGAT------TTT 157

Qy         39 ProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThr 58
                 :::      ||||||:::||||||||||||||||:::::::|||   |||||||||
Db        158 AACCGAGGCACGGACAACATCACCGTGAGGCAGGGGGACACGGCCATCCTCAGGTGTGTG 217

Qy         59 IleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGly 78
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Db        218 GTAGAAGACAAGAACTCGAAAGTGGCCTGGTTGAACCGCTCTGGCATCATCTTCGCTGGA 277

Qy         79 AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyr 98

Db        278 CACGACAAGTGGTCTCTGGACCCTCGGGTTGAGCTGGAGAAACGCCATGCTCTGGAATAC 337

Qy         99 SerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGln 118

Db        338 AGCCTCCGAATCCAGAAGGTGGATGTCTATGATGAAGGATCCTACACATGCTCAGTTCAG 397

Qy        119 ThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle 138

Db        398 ACACAGCATGAGCCCAAGACCTCTCAAGTTTACTTGATTGTACAAGTTCCACCAAAGATC 457

Qy        139 ValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIle 158

Db        458 TCCAACATCTCCTCGGATGTCACTGTGAATGAGGGCAGCAATGTAACCCTGGTCTGCATG 517

Qy        159 AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly 178

Db        518 GCCAATGGGCGCCCTGAACCTGTTATCACCTGGAGACACCTTACACCACTTGGAAGAGAA 577

Qy        179 PheValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAsp 198

Db        578 TTTGAAGGAGAAGAAGAATATCTGGAGATCCTAGGCATCACCAGGGAACAGTCAGGCAAA 637

Qy        199 TyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThr 218

Db        638 TATGAGTGCAAGGCTGCCAACGAGGTCTCCTCCGCGGATGTCAAACAAGTCAAGGTCACT 697

Qy        219 ValAsnTyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLys 238

Db        698 GTGAACTATCCACCCACCATCACAGAGTCTAAGAGCAATGAAGCCACCACAGGACGACAA 757

Qy        239 GlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAsp 258

Db        758 GCTTCCCTCAAATGTGAAGCCTCAGCGGTGCCTGCACCTGACTTTGAGTGGTACCGGGAT 817

Qy        259 AspLysArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSer 278

Db        818 GACACCAGG---ATAAACAGTGCAAACGGCCTTGAGATTAAGAGCACTGAGGGCCAGTCC 874

Qy        279 LysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSer 298

Db        875 TCCCTGACGGTGACCAACGTCACTGAGGAACACTACGGCAACTATACCTGTGTGGCTGCC 934

Qy        299 AsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGlu 318

Db        935 AACAAGCTCGGCGTCACCAATGCCAGCCTAGTCCTTTTCAGACCCGGGTCGGTGAGAGGA 994

Qy        319 ValSerAsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeu 338

Db        995 ATC---AACGGATCCATCAGTCTGGCCGTACCACTGTGGCTGCTGGCAGCGTCCCTGTTC 1051

Qy        339 HisLeuLeuLeuLys 343

Db       1052 TGCCTTCTCAGCAAA 1066

RESULT 4
US-09-135-080-3
; Sequence 3, Application US/09135080
; Patent No. 6423827
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat R.
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/135,080
;      FILING DATE:  17-AUG-1998
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/414,657
;      FILING DATE:  31-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-620-3214
;      TELEFAX:  609-620-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1238 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  56...1069
;      OTHER INFORMATION:
US-09-135-080-3

Alignment Scores:
Pred. No.:              6.2e-99        Length:          1238
Score:                  926.50         Matches:         179
Percent Similarity:     73.54%         Conservative:    60
Best Local Similarity:  55.08%         Mismatches:      81
Query Match:            51.30%         Indels:          5
DB:                     4              Gaps:            4

US-10-017-084A-523 (1-344) x US-09-135-080-3 (1-1238)

Qy         20 LeuAlaAlaLeuCysLeuPhe---GlnGlyValProValArgSerGlyAspAlaThrPhe 38

Db        104 CTGAGACTGCTCTGCCTTCTTCCCACAGGACTGCCCGTTCGCAGCGTGGAT------TTT 157

Qy         39 ProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThr 58

Db        158 AACCGAGGCACGGACAACATCACCGTGAGGCAGGGGGACACGGCCATCCTCAGGTGTGTG 217

Qy         59 IleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGly 78

Db        218 GTAGAAGACAAGAACTCGAAAGTGGCCTGGTTGAACCGCTCTGGCATCATCTTCGCTGGA 277

Qy         79 AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyr 98

Db        278 CACGACAAGTGGTCTCTGGACCCTCGGGTTGAGCTGGAGAAACGCCATGCTCTGGAATAC 337

Qy         99 SerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGln 118

Db        338 AGCCTCCGAATCCAGAAGGTGGATGTCTATGATGAAGGATCCTACACATGCTCAGTTCAG 397

Qy        119 ThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle 138

Db        398 ACACAGCATGAGCCCAAGACCTCTCAAGTTTACTTGATTGTACAAGTTCCACCAAAGATC 457

Qy        139 ValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIle 158
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Db        458 TCCAACATCTCCTCGGATGTCACTGTGAATGAGGGCAGCAATGTAACCCTGGTCTGCATG 517

Qy        159 AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly 178

Db        518 GCCAATGGGCGCCCTGAACCTGTTATCACCTGGAGACACCTTACACCACTTGGAAGAGAA 577

Qy        179 PheValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAsp 198

Db        578 TTTGAAGGAGAAGAAGAATATCTGGAGATCCTAGGCATCACCAGGGAACAGTCAGGCAAA 637

Qy        199 TyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThr 218

Db        638 TATGAGTGCAAGGCTGCCAACGAGGTCTCCTCCGCGGATGTCAAACAAGTCAAGGTCACT 697

Qy        219 ValAsnTyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLys 238

Db        698 GTGAACTATCCACCCACCATCACAGAGTCTAAGAGCAATGAAGCCACCACAGGACGACAA 757

Qy        239 GlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAsp 258

Db        758 GCTTCCCTCAAATGTGAAGCCTCAGCGGTGCCTGCACCTGACTTTGAGTGGTACCGGGAT 817

Qy        259 AspLysArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSer 278

Db        818 GACACCAGG---ATAAACAGTGCAAACGGCCTTGAGATTAAGAGCACTGAGGGCCAGTCC 874

Qy        279 LysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSer 298

Db        875 TCCCTGACGGTGACCAACGTCACTGAGGAACACTACGGCAACTATACCTGTGTGGCTGCC 934

Qy        299 AsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGlu 318

Db        935 AACAAGCTCGGCGTCACCAATGCCAGCCTAGTCCTTTTCAGACCCGGGTCGGTGAGAGGA 994

Qy        319 ValSerAsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeu 338

Db        995 ATC---AACGGATCCATCAGTCTGGCCGTACCACTGTGGCTGCTGGCAGCGTCCCTGTTC 1051

Qy        339 HisLeuLeuLeuLys 343

Db       1052 TGCCTTCTCAGCAAA 1066

RESULT 5
US-08-414-657D-1
; Sequence 1, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  977 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  2...976
;      OTHER INFORMATION:
US-08-414-657D-1

Alignment Scores:
Pred. No.:                9.62e-99        Length:          977
Score:                    923.50          Matches:         177
Percent Similarity:       74.06%          Conservative:    60
Best Local Similarity:    55.31%          Mismatches:      78
Query Match:              51.14%          Indels:          5
DB:                       2               Gaps:            4

US-10-017-084A-523 (1-344) x US-08-414-657D-1 (1-977)

Qy         20 LeuAlaAlaLeuCysLeuPhe---GlnGlyValProValArgSerGlyAspAlaThrPhe 38

Db         29 CTGAGATTGCTCTGCCTTCTTCCCACAGGACTGCCTGTTCGCAGCGTGGAT------TTT 82

Qy         39 ProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThr 58

Db         83 AACCGAGGCACGGACAACATCACCGTGAGGCAGGGGGACACAGCCATCCTCAGGTGCGTT 142

Qy         59 IleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGly 78

Db        143 CTAGAAGACAAGAACTCAAAGGTGGCCTGGTTGAACCGTTCTGGCATCATTTTTGCTGGA 202

Qy         79 AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyr 98

Db        203 CATGACAAGTGGTCTCTGGACCCACGGGTTGAGCTGGAGAAACGCCATTCTCTGGAATAC 262

Qy         99 SerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGln 118

Db        263 AGCCTCCGAATCCAGAAGGTGGATGTCTATGATGAGGGTTCCTACACTTGCTCAGTTCAG 322

Qy        119 ThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle 138

Db        323 ACACAGCATGAGCCCAAGACCTCCCAAGTTTACTTGATCGTACAAGTCCCACCAAAGATC 382

Qy        139 ValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIle 158

Db        383 TCCAATATCTCCTCGGATGTCACTGTGAATGAGGGCAGCAACGTGACTCTGGTCTGCATG 442

Qy        159 AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly 178

Db        443 GCCAATGGCCGTCCTGAACCTGTTATCACCTGGAGACACCTTACACCAACTGGAAGGGAA 502

Qy        179 PheValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAsp 198

Db        503 TTTGAAGGAGAAGAAGAATATCTGGAGATCCTTGGCATCACCAGGGAGCAGTCAGGCAAA 562

Qy        199 TyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThr 218

Db        563 TATGAGTGCAAAGCTGCCAACGAGGTCTCCTCGGCGGATGTCAAACAAGTCAAGGTCACT 622

Qy        219 ValAsnTyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLys 238

Db        623 GTGAACTATCCTCCCACTATCACAGAATCCAAGAGCAATGAAGCCACCACAGGACGACAA 682
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Qy        239 GlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAsp 258
              :::|||:::|||||||||||||||||||||||::   :::|||:::||||||:::|||
Db        683 GCTTCACTCAAATGTGAGGCCTCGGCAGTGCCTGCACCTGACTTTGAGTGGTACCGGGAT 742

Qy        259 AspLysArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSer 278
              |||   |||   |||           |||:::::::::::::::           |||
Db        743 GACACTAGG---ATAAATAGTGCCAATGGCCTTGAGATTAAGAGCACGGAGGGCCAGTCT 799

Qy        279 LysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSer 298
              |||         ||||||:::|||    ||||||||||||||||||||||||:::
Db        800 TCCCTGACGGTGACCAACGTCACTGAGGAGCACTACGGCAACTACACCTGTGTGGCTGCC 859

Qy        299 AsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGlu 318
              ||||||||||||   ||||||||||||:::::||||||   ||||||:::|||
Db        860 AACAAGCTGGGGGTCACCAATGCCAGCCTAGTCCTTTTCAGACCTGGGTCGGTGAGAGGA 919

Qy        319 ValSerAsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeu 338
              :::   ||||||:::        |||     :::||||||||||        :::|||
Db        920 ATA---AATGGATCCATCAGTCTGGCCGTACCACTGTGGCTGCTGGCAGCATCTCTGCTC 976

RESULT 6
US-09-135-080-1
; Sequence 1, Application US/09135080
; Patent No. 6423827
; GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat R.
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/135,080
;      FILING DATE:  17-AUG-1998
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/414,657
;      FILING DATE:  31-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-620-3214
;      TELEFAX:  609-620-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  977 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  2...976
;      OTHER INFORMATION:
US-09-135-080-1

Alignment Scores:

Pred. No.:              9.62e-99        Length:         977
Score:                  923.50          Matches:        177
Percent Similarity:     74.06%          Conservative:   60
Best Local Similarity:  55.31%          Mismatches:     78
Query Match:            51.14%          Indels:         5
DB:                     4               Gaps:           4

US-10-017-084A-523 (1-344) x US-09-135-080-1 (1-977)

Qy         20 LeuAlaAlaLeuCysLeuPhe---GlnGlyValProValArgSerGlyAspAlaThrPhe 38
              |||      |||||||||          |||:::|||||||||||||   |||      |||
Db         29 CTGAGATTGCTCTGCCTTCTTCCCACAGGACTGCCTGTTCGCAGCGTGGAT------TTT 82

Qy         39 ProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThr 58
              :::     ||||||:::|||||||||||||||:::::|||   |||||||||
Db         83 AACCGAGGCACGGACAACATCACCGTGAGGCAGGGGGACACAGCCATCCTCAGGTGCGTT 142

Qy         59 IleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGly 78
              ::::::::::::   ::::::||||||||||||||||||||||   |||:::::||||||
Db        143 CTAGAAGACAAGAACTCAAAGGTGGCCTGGTTGAACCGTTCTGGCATCATTTTTGCTGGA 202

Qy         79 AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyr 98
              :::|||||||||   ||||||||||||||   |||                  :::|||
Db        203 CATGACAAGTGGTCTCTGGACCCACGGGTTGAGCTGGAGAAACGCCATTCTCTGGAATAC 262

Qy         99 SerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGln 118
              |||:::   ||||||   ||||||||||||||||||||||   ||||||||||||||||||
Db        263 AGCCTCCGAATCCAGAAGGTGGATGTCTATGATGAGGGTTCCTACACTTGCTCAGTTCAG 322

Qy        119 ThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle 138
              |||   :::   ||||||||||||:::|||:::||||||||||||||   |||||||||
Db        323 ACACAGCATGAGCCCAAGACCTCCCAAGTTTACTTGATCGTACAAGTCCCACCAAAGATC 382

Qy        139 ValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIle 158
              ||||||||||||:::::::::|||||||||:::|||:::::::|||   ||||::
Db        383 TCCAATATCTCCTCGGATGTCACTGTGAATGAGGGCAGCAACGTGACTCTGGTCTGCATG 442

Qy        159 AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly 178
              |||   ||||||||||||||   :::||||||||||||:::::::|||
Db        443 GCCAATGGCCGTCCTGAACCTGTTATCACCTGGAGACACCTTACACCAACTGGAAGGGAA 502

Qy        179 PheValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAsp 198
              |||      |||:::||||||||||||||   ||||||||||||||||||||||||
Db        503 TTTGAAGGAGAAGAAGAATATCTGGAGATCCTTGGCATCACCAGGGAGCAGTCAGGCAAA 562

Qy        199 TyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThr 218
              |||||||||   |||:::|||:::|||::::::      |||:::::::||||||||||||
Db        563 TATGAGTGCAAAGCTGCCAACGAGGTCTCCTCGGCGGATGTCAAACAAGTCAAGGTCACT 622

Qy        219 ValAsnTyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLys 238
              ||||||||||||||   |||:::|||:::|||                  |||::::::
Db        623 GTGAACTATCCTCCCACTATCACAGAATCCAAGAGCAATGAAGCCACCACAGGACGACAA 682

Qy        239 GlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAsp 258
              :::|||:::|||||||||||||||||||||||::   :::|||:::||||||:::|||
Db        683 GCTTCACTCAAATGTGAGGCCTCGGCAGTGCCTGCACCTGACTTTGAGTGGTACCGGGAT 742

Qy        259 AspLysArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSer 278
              |||   |||   |||           |||:::::::::::::::           |||
Db        743 GACACTAGG---ATAAATAGTGCCAATGGCCTTGAGATTAAGAGCACGGAGGGCCAGTCT 799

Qy        279 LysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSer 298
              |||         ||||||:::|||    ||||||||||||||||||||||||:::
Db        800 TCCCTGACGGTGACCAACGTCACTGAGGAGCACTACGGCAACTACACCTGTGTGGCTGCC 859

Qy        299 AsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGlu 318
              ||||||||||||   ||||||||||||:::::||||||   ||||||:::|||
Db        860 AACAAGCTGGGGGTCACCAATGCCAGCCTAGTCCTTTTCAGACCTGGGTCGGTGAGAGGA 919

Qy        319 ValSerAsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeu 338
              :::   ||||||:::        |||     :::||||||||||        :::|||
Db        920 ATA---AATGGATCCATCAGTCTGGCCGTACCACTGTGGCTGCTGGCAGCATCTCTGCTC 976
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RESULT 7
US-08-414-657D-7
; Sequence 7, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  924 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...924
;      OTHER INFORMATION:
US-08-414-657D-7

Alignment Scores:
Pred. No.:              5.8e-97      Length:          924
Score:                  908.00       Matches:         170
Percent Similarity:     75.50%       Conservative:    58
Best Local Similarity:  56.29%       Mismatches:      70
Query Match:            50.28%       Indels:          4
DB:                     2            Gaps:            3

US-10-017-084A-523 (1-344) x US-08-414-657D-7 (1-924)

Qy         20 LeuAlaAlaLeuCysLeuPhe---GlnGlyValProValArgSerGlyAspAlaThrPhe 38
              |||      |||||||||         |||:::|||||||||||||   |||      |||
Db         28 CTGAGATTGCTCTGCCTTCTTCCCACAGGACTGCCTGTTCGCAGCGTGGAT------TTT 81

Qy         39 ProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThr 58
                 :::      ||||||:::|||||||||||||||:::::|||   |||||||||
Db         82 AACCGAGGCACGGACAACATCACCGTGAGGCAGGGGGACACAGCCATCCTCAGGTGCGTT 141

Qy         59 IleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGly 78
              ::::::::::::   ::::::|||||||||||||||||||||   |||:::::||||||
Db        142 CTAGAAGACAAGAACTCAAAGGTGGCCTGGTTGAACCGTTCTGGCATCATTTTTGCTGGA 201

Qy         79 AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyr 98
              :::||||||||||   |||||||||||||||   |||                :::|||
Db        202 CATGACAAGTGGTCTCTGGACCCACGGGTTGAGCTGGAGAAACGCCATTCTCTGGAATAC 261

Qy         99 SerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGln 118
              |||:::   ||||||   ||||||||||||||||||||||   ||||||||||||||||||
Db        262 AGCCTCCGAATCCAGAAGGTGGATGTCTATGATGAGGGTTCCTACACTTGCTCAGTTCAG 321

Qy        119 ThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle 138
              |||   :::   |||||||||||||:::|||:::||||||||||||||   |||||||||
Db        322 ACACAGCATGAGCCCAAGACCTCCCAAGTTTACTTGATCGTACAAGTCCCACCAAAGATC 381

Qy        139 ValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIle 158
                 ||||||||||||:::::::::|||||||||:::|||:::::::|||   |||:::
Db        382 TCCAATATCTCCTCGGATGTCACTGTGAATGAGGGCAGCAACGTGACTCTGGTCTGCATG 441

Qy        159 AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly 178
              |||   ||||||||||||||   :::|||||||||||||:::::|||
Db        442 GCCAATGGCCGTCCTGAACCTGTTATCACCTGGAGACACCTTACACCAACTGGAAGGGAA 501

Qy        179 PheValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAsp 198
              |||      ||:::||||||||||||   ||||||||||||||||||||||
Db        502 TTTGAAGGAGAAGAAGAATATCTGGAGATCCTTGGCATCACCAGGGAGCAGTCAGGCAAA 561

Qy        199 TyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThr 218
              |||||||||   |||:::|||:::|||:::::      |||:::::|||||||||||||
Db        562 TATGAGTGCAAAGCTGCCAACGAGGTCTCCTCGGCGGATGTCAAACAAGTCAAGGTCACT 621

Qy        219 ValAsnTyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLys 238
              ||||||||||||||   |||:::|||:::|||                  |||:::::::
Db        622 GTGAACTATCCTCCCACTATCACAGAATCCAAGAGCAATGAAGCCACCACAGGACGACAA 681

Qy        239 GlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAsp 258
                 :::|||:::|||||||||||||||||||||||:::   :::|||:::|||||:::|||
Db        682 GCTTCACTCAAATGTGAGGCCTCGGCAGTGCCTGCACCTGACTTTGAGTGGTACCGGGAT 741

Qy        259 AspLysArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSer 278
              |||   |||   |||            |||:::::::::::::::            |||
Db        742 GACACTAGG---ATAAATAGTGCCAATGGCCTTGAGATTAAGAGCACGGAGGGCCAGTCT 798

Qy        279 LysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSer 298
                 |||        ||||||:::|||      ||||||||||||||||||||||||:::
Db        799 TCCCTGACGGTGACCAACGTCACTGAGGAGCACTACGGCAACTACACCTGTGTGGCTGCC 858

Qy        299 AsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGlu 318
              ||||||||||||   ||||||||||||:::::||||||   |||||||:::|||
Db        859 AACAAGCTGGGGGTCACCAATGCCAGCCTAGTCCTTTTCAGACCTGGGTCGGTGAGAGGA 918

Qy        319 ValSer 320
              ::::::
Db        919 ATAAAT 924

RESULT 8
US-08-414-657D-8
; Sequence 8, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
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;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  945 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...945
;      OTHER INFORMATION:
US-08-414-657D-8

Alignment Scores:
Pred. No.:              7.87e-97        Length:         945
Score:                  907.00          Matches:        170
Percent Similarity:     75.50%          Conservative:   58
Best Local Similarity:  56.29%          Mismatches:     70
Query Match:            50.22%          Indels:         4
DB:                     2               Gaps:           3

US-10-017-084A-523 (1-344) x US-08-414-657D-8 (1-945)

Qy         20 LeuAlaAlaLeuCysLeuPhe---GlnGlyValProValArgSerGlyAspAlaThrPhe 38
              |||      ||||||||||         |||:::|||||||||||||||   |||      |||
Db         49 CTGAGACTGCTCTGCCTTCTTCCCACAGGACTGCCCGTTCGCAGCGTGGAT------TTT 102

Qy         39 ProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThr 58
                 :::    ||||||:::||||||||||||||||:::::|||   ||||||||
Db        103 AACCGAGGCACGGACAACATCACCGTGAGGCAGGGGGACACGGCCATCCTCAGGTGTGTG 162

Qy         59 IleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGly 78
              ::::::::::::   :::::::||||||||||||||||||||   |||::::::||||||
Db        163 GTAGAAGACAAGAACTCGAAAGTGGCCTGGTTGAACCGCTCTGGCATCATCTTCGCTGGA 222

Qy         79 AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyr 98
              :::||||||||||   ||||||||||||||   |||                  :::|||
Db        223 CACGACAAGTGGTCTCTGGACCCTCGGGTTGAGCTGGAGAAACGCCATGCTCTGGAATAC 282

Qy         99 SerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGln 118
              |||:::   ||||||   ||||||||||||||||||||   ||||||||||||||||||
Db        283 AGCCTCCGAATCCAGAAGGTGGATGTCTATGATGAAGGATCCTACACATGCTCAGTTCAG 342

Qy        119 ThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle 138
              |||   :::  ||||||||||||:::|||:::||||||||||||||||   |||||||||
Db        343 ACACAGCATGAGCCCAAGACCTCTCAAGTTTACTTGATTGTACAAGTTCCACCAAAGATC 402

Qy        139 ValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIle 158
                     ||||||||||:::::::::||||||||:::|||:::::::|||   |||:::
Db        403 TCCAACATCTCCTCGGATGTCACTGTGAATGAGGGCAGCAATGTAACCCTGGTCTGCATG 462

Qy        159 AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly 178
              |||   ||||||||||||||   :::||||||||||||:::::::|||
Db        463 GCCAATGGGCGCCCTGAACCTGTTATCACCTGGAGACACCTTACACCACTTGGAAGAGAA 522

Qy        179 PheValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAsp 198
                 |||      ||:::|||||||||||||||   ||||||||||||||||||||||||
Db        523 TTTGAAGGAGAAGAAGAATATCTGGAGATCCTAGGCATCACCAGGGAACAGTCAGGCAAA 582

Qy        199 TyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThr 218
              |||||||||   |||:::|||:::|||::::::      |||:::::|||||||||||||
Db        583 TATGAGTGCAAGGCTGCCAACGAGGTCTCCTCCGCGGATGTCAAACAAGTCAAGGTCACT 642

Qy        219 ValAsnTyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLys 238
              ||||||||||||||   |||:::|||:::|||                  |||:::::::
Db        643 GTGAACTATCCACCCACCATCACAGAGTCTAAGAGCAATGAAGCCACCACAGGACGACAA 702

Qy        239 GlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAsp 258
              :::|||:::|||||||||||||||||||||:::   :::|||:::|||||||:::|||
Db        703 GCTTCCCTCAAATGTGAAGCCTCAGCGGTGCCTGCACCTGACTTTGAGTGGTACCGGGAT 762

Qy        259 AspLysArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSer 278
              |||  |||  |||            |||:::::::::::::::                |||
Db        763 GACACCAGG--ATAAACAGTGCAAACGGCCTTGAGATTAAGAGCACTGAGGGCCAGTCC 819

Qy        279 LysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSer 298
                 |||         ||||||:::|||      |||||||||||||||||||||||:::
Db        820 TCCCTGACGGTGACCAACGTCACTGAGGAACACTACGGCAACTATACCTGTGTGGCTGCC 879

Qy        299 AsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGlu 318
              ||||||||||||   ||||||||||||:::::||||||   ||||||:::|||
Db        880 AACAAGCTCGGCGTCACCAATGCCAGCCTAGTCCTTTTCAGACCCGGGTCGGTGAGAGGA 939

Qy        319 ValSer 320
              ::::::
Db        940 ATCAAC 945

RESULT 9
US-08-414-657D-6
; Sequence 6, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  912 base pairs
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;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...912
;      OTHER INFORMATION:
US-08-414-657D-6

Alignment Scores:
Pred. No.:              2.87e-96        Length:         912
Score:                  902.00          Matches:        171
Percent Similarity:     74.68%          Conservative:   59
Best Local Similarity:  55.52%          Mismatches:     74
Query Match:            49.94%          Indels:         4
DB:                     2               Gaps:           3

US-10-017-084A-523 (1-344) x US-08-414-657D-6 (1-912)

Qy         31 ValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArgGlnGly 50
              |||||||||   |||      |||   :::     ||||||:::|||||||||||||||||
Db          1 GTTCGCAGCGTGGAT------TTTAACCGAGGCACGGACAACATCACCGTGAGGCAGGGG 54

Qy         51 GluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsn 70
              ::::::|||   |||||||||   ::::::::::::   ::::::|||||||||||||||
Db         55 GACACAGCCATCCTCAGGTGCGTTCTAGAAGACAAGAACTCAAAGGTGGCCTGGTTGAAC 114

Qy         71 ArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeu 90
              ||||||   |||::::::|||||||:::|||||||||   |||||||||||||||   |||
Db        115 CGTTCTGGCATCATTTTTGCTGGACATGACAAGTGGTCTCTGGACCCACGGGTTGAGCTG 174

Qy         91 LeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyrAspGlu 110
                        :::|||||||:::   ||||||   ||||||||||||||||||
Db        175 GAGAAACGCCATTCTCTGGAATACAGCCTCCGAATCCAGAAGGTGGATGTCTATGATGAG 234

Qy        111 GlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeu 130
              |||   ||||||||||||||||||||   :::   ||||||||||||:::|||:::|||
Db        235 GGTTCCTACACTTGCTCAGTTCAGACACAGCATGAGCCCAAGACCTCCCAAGTTTACTTG 294

Qy        131 IleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGly 150
              ||||||||||||   |||||||||      ||||||||||:::::::::|||||||||
Db        295 ATCGTACAAGTCCCACCAAAGATCTCCAATATCTCCTCGGATGTCACTGTGAATGAGGGC 354

Qy        151 AsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArg 170
              :::|||:::::|||   |||:::|||   ||||||||||||||   :::|||||||||
Db        355 AGCAACGTGACTCTGGTCTGCATGGCCAATGGCCGTCCTGAACCTGTTATCACCTGGAGA 414

Qy        171 HisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGly 190
              |||::::::|||            |||      |||:::|||||||||||||||   |||
Db        415 CACCTTACACCAACTGGAAGGGAATTTGAAGGAGAAGAAGAATATCTGGAGATCCTTGGC 474

Qy        191 IleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaPro 210
              ||||||||||||||||||||   |||||||||   |||:::|||:::|||::::::
Db,       475 ATCACCAGGGAGCAGTCAGGCAAATATGAGTGCAAAGCTGCCAACGAGGTCTCCTCGGCG 534

Qy        211 ValValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGly 230
              |||::::::|||||||||||||||||||||||||||||   |||:::|||:::|||
Db        535 GATGTCAAACAAGTCAAGGTCACTGTGAACTATCCTCCCACTATCACAGAATCCAAGAGC 594

Qy        231 ThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSer 250
                          |||::::::   :::|||:::|||||||||||||||||||||||:::
Db        595 AATGAAGCCACCACAGGACGACAAGCTTCACTCAAATGTGAGGCCTCGGCAGTGCCTGCA 654

Qy        251 AlaGluPheGlnTrpTyrLysAspAspLysArgLeuIleGluGlyLysLysGlyValLys 270
              :::|||:::||||||:::||||||   |||   |||            |||::::::
Db        655 CCTGACTTTGAGTGGTACCGGGATGACACTAGG---ATAAATAGTGCCAATGGCCTTGAG 711

Qy        271 ValGluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyr 290
              :::::::::          |||   |||         |||||:::|||      |||
Db        712 ATTAAGAGCACGGAGGGCCAGTCTTCCCTGACGGTGACCAACGTCACTGAGGAGCACTAC 771

Qy        291 GlyAsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeu 310
              ||||||||||||||||||||:::||||||||||||   |||||||||||:::::|||

Db        772 GGCAACTACACCTGTGTGGCTGCCAACAAGCTGGGGGTCACCAATGCCAGCCTAGTCCTT 831

Qy        311 PheGlyProGlyAlaValSerGluValSerAsnGlyThrSerArgArgAlaGlyCysVal 330
              |||   ||||||:::|||      :::   |||||||:::         |||      :::
Db        832 TTCAGACCTGGGTCGGTGAGAGGAATA---AATGGATCCATCAGTCTGGCCGTACCACTG 888

Qy        331 TrpLeuLeuProLeuLeuValLeu 338
              |||||||||          :::|||
Db        889 TGGCTGCTGGCAGCATCTCTGCTC 912

RESULT 10
US-08-414-657D-9
; Sequence 9, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  861 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...861
;      OTHER INFORMATION:
US-08-414-657D-9

Alignment Scores:
Pred. No.:              1.73e-94        Length:         861
Score:                  886.50          Matches:        164
Percent Similarity:     76.21%          Conservative:   57
Best Local Similarity:  56.55%          Mismatches:     66
Query Match:            49.09%          Indels:         3
DB:                     2               Gaps:           2

US-10-017-084A-523 (1-344) x US-08-414-657D-9 (1-861)

Qy         31 ValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArgGlnGly 50
              |||||||||   |||      |||   :::     ||||||:::|||||||||||||||||
```

```
Db          1 GTTCGCAGCGTGGAT------TTTAACCGAGGCACGGACAACATCACCGTGAGGCAGGGG 54

Qy         51 GluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsn 70
              :::::|||   |||||||||   ::::::::::::   ::::::|||||||||||||||||
Db         55 GACACAGCCATCCTCAGGTGCGTTCTAGAAGACAAGAACTCAAAGGTGGCCTGGTTGAAC 114

Qy         71 ArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeu 90
              ||||||   |||::::::|||||||:::|||||||||   |||||||||||||||   |||
Db        115 CGTTCTGGCATCATTTTTGCTGGACATGACAAGTGGTCTCTGGACCCACGGGTTGAGCTG 174

Qy         91 LeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyrAspGlu 110
                          :::|||||||:::   ||||||   ||||||||||||||||||||
Db        175 GAGAAACGCCATTCTCTGGAATACAGCCTCCGAATCCAGAAGGTGGATGTCTATGATGAG 234

Qy        111 GlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeu 130
              |||   ||||||||||||||||||||||   :::   ||||||||||||:::|||:::|||
Db        235 GGTTCCTACACTTGCTCAGTTCAGACACAGCATGAGCCCAAGACCTCCCAAGTTTACTTG 294

Qy        131 IleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGly 150
              ||||||||||||   |||||||||      ||||||||||||:::::::::|||||||||
Db        295 ATCGTACAAGTCCCACCAAAGATCTCCAATATCTCCTCGGATGTCACTGTGAATGAGGGC 354

Qy        151 AsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArg 170
              :::|||::::::|||   |||:::|||   .|||||||||||||   :::|||||||||.
Db        355 AGCAACGTGACTCTGGTCTGCATGGCCAATGGCCGTCCTGAACCTGTTATCACCTGGAGA 414

Qy        171 HisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGly 190
              |||::::::|||            |||      |||:::|||||||||||||||   |||
Db        415 CACCTTACACCAACTGGAAGGGAATTTGAAGGAGAAGAAGAATATCTGGAGATCCTTGGC 474

Qy        191 IleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaPro 210
              ||||||||||||||||||||   |||||||||   |||:::|||:::|||::::::
Db        475 ATCACCAGGGAGCAGTCAGGCAAATATGAGTGCAAAGCTGCCAACGAGGTCTCCTCGGCG 534

Qy        211 ValValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGly 230
                 |||::::::|||||||||||||||||||||||||||||   |||:::|||:::|||
Db        535 GATGTCAAACAAGTCAAGGTCACTGTGAACTATCCTCCCACTATCACAGAATCCAAGAGC 594

Qy        231 ThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSer 250
                          |||:::::::   :::|||:::|||||||||||||||||||||:::
Db        595 AATGAAGCCACCACAGGACGACAAGCTTCACTCAAATGTGAGGCCTCGGCAGTGCCTGCA 654

Qy        251 AlaGluPheGlnTrpTyrLysAspAspLysArgLeuIleGluGlyLysLysGlyValLys 270
                 :::|||:::|||||||:::|||||||   |||   |||                |||::::::
Db        655 CCTGACTTTGAGTGGTACCGGGATGACACTAGG---ATAAATAGTGCCAATGGCCTTGAG 711

Qy        271 ValGluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyr 290
              :::::::::          |||   |||          |||||||:::|||      |||
Db        712 ATTAAGAGCACGGAGGGCCAGTCTTCCCTGACGGTGACCAACGTCACTGAGGAGCACTAC 771

Qy        291 GlyAsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeu 310
              |||||||||||||||||||||:::||||||||||||   ||||||||||||:::::::|||
Db        772 GGCAACTACACCTGTGTGGCTGCCAACAAGCTGGGGGTCACCAATGCCAGCCTAGTCCTT 831

Qy        311 PheGlyProGlyAlaValSerGluValSer 320
              |||   ||||||:::|||      ::::::
Db        832 TTCAGACCTGGGTCGGTGAGAGGAATAAAT 861

RESULT 11
US-08-414-657D-10
; Sequence 10, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  861 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...861
;      OTHER INFORMATION:
US-08-414-657D-10

Alignment Scores:
Pred. No.:                2.26e-94        Length:          861
Score:                    885.50          Matches:         164
Percent Similarity:       76.21%          Conservative:    57
Best Local Similarity:    56.55%          Mismatches:      66
Query Match:              49.03%          Indels:          3
DB:                       2               Gaps:            2

US-10-017-084A-523 (1-344) x US-08-414-657D-10 (1-861)

Qy         31 ValArgSerGlyAspAlaThrProProLysAlaMetAspAsnValThrValArgGlnGly 50
              |||||||||   |||      |||   :::      ||||||:::|||||||||||||||||
Db          1 GTTCGCAGCGTGGAT------TTTAACCGAGGCACGGACAACATCACCGTGAGGCAGGGG 54

Qy         51 GluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsn 70
              :::::|||   |||||||||   ::::::::::::   ::::::|||||||||||||||||
Db         55 GACACGGCCATCCTCAGGTGTGTGGTAGAAGACAAGAACTCGAAAGTGGCCTGGTTGAAC 114

Qy         71 ArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeu 90
              ||||||   |||:::::::|||||||:::|||||||||   |||||||||||||||   |||
Db        115 CGCTCTGGCATCATCTTCGCTGGACACGACAAGTGGTCTCTGGACCCTCGGGTTGAGCTG 174

Qy         91 LeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyrAspGlu 110
                          :::|||||||:::   ||||||   ||||||||||||||||||||
Db        175 GAGAAACGCCATGCTCTGGAATACAGCCTCCGAATCCAGAAGGTGGATGTCTATGATGAA 234

Qy        111 GlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeu 130
              |||   ||||||||||||||||||||||   :::   ||||||||||||:::|||:::|||
Db        235 GGATCCTACACATGCTCAGTTCAGACACAGCATGAGCCCAAGACCTCTCAAGTTTACTTG 294

Qy        131 IleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGly 150
              ||||||||||||   |||||||||      ||||||||||||:::::::::|||||||||
Db        295 ATTGTACAAGTTCCACCAAAGATCTCCAACATCTCCTCGGATGTCACTGTGAATGAGGGC 354

Qy        151 AsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArg 170
              :::|||::::::|||   |||:::|||   |||||||||||||   :::|||||||||.
Db        355 AGCAATGTAACCCTGGTCTGCATGGCCAATGGGCGCCCTGAACCTGTTATCACCTGGAGA 414
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Qy        171 HisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGly 190
              |||:::::::|||          |||     |||:::|||||||||||||||||   |||
Db        415 CACCTTACACCACTTGGAAGAGAATTTGAAGGAGAAGAAGAATATCTGGAGATCCTAGGC 474

Qy        191 IleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaPro 210
              ||||||||||||||||||||   |||||||||   |||:::|||:::|||::::::
Db        475 ATCACCAGGGAACAGTCAGGCAAATATGAGTGCAAGGCTGCCAACGAGGTCTCCTCCGCG 534

Qy        211 ValValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGly 230
                 |||:::::::|||||||||||||||||||||||||||||   |||:::|||:::|||
Db        535 GATGTCAAACAAGTCAAGGTCACTGTGAACTATCCACCCACCATCACAGAGTCTAAGAGC 594

Qy        231 ThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSer 250
                          |||:::::::   :::|||:::|||||||||||||||||||||||:::
Db        595 AATGAAGCCACCACAGGACGACAAGCTTCCCTCAAATGTGAAGCCTCAGCGGTGCCTGCA 654

Qy        251 AlaGluPheGlnTrpTyrLysAspAspLysArgLeuIleGluGlyLysLysGlyValLys 270
              :::|||:::||||||:::||||||   |||  |||              |||::::::
Db        655 CCTGACTTTGAGTGGTACCGGGATGACACCAGG---ATAAACAGTGCAAACGGCCTTGAG 711

Qy        271 ValGluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyr 290
              :::::::::            |||   |||         ||||||:::|||      |||
Db        712 ATTAAGAGCACTGAGGGCCAGTCCTCCCTGACGGTGACCAACGTCACTGAGGAACACTAC 771

Qy        291 GlyAsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeu 310
              ||||||||||||||||||||:::|||||||||||   ||||||||||||:::::|||
Db        772 GGCAACTATACCTGTGTGGCTGCCAACAAGCTCGGCGTCACCAATGCCAGCCTAGTCCTT 831

Qy        311 PheGlyProGlyAlaValSerGluValSer 320
              |||   ||||||:::|||      :::::
Db        832 TTCAGACCCGGGTCGGTGAGAGGAATCAAC 861

RESULT 12
US-08-414-657D-17
; Sequence 17, Application US/08414657D
; Patent No. 5851283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  756 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...756
;      OTHER INFORMATION:
US-08-414-657D-17

Alignment Scores:
Pred. No.:              5.09e-84        Length:         756
Score:                  796.50          Matches:        144
Percent Similarity:     76.68%          Conservative:   50
Best Local Similarity:  56.92%          Mismatches:     58
Query Match:            44.10%          Indels:         1
DB:                     2               Gaps:           1

US-10-017-084A-523 (1-344) x US-08-414-657D-17 (1-756)

Qy         50 GlyGluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeu 69
              |||:::::|||   |||||||||   ::::::::::::   ::::::||||||||||||
Db          1 GGGGACACAGCCATCCTCAGGTGCGTTCTAGAAGACAAGAACTCAAAGGTGGCCTGGTTG 60

Qy         70 AsnArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgValVal 89
              |||||||||   |||:::::|||||:::|||||||||   ||||||||||||||||
Db         61 AACCGTTCTGGCATCATTTTTGCTGGACATGACAAGTGGTCTCTGGACCCACGGGTTGAG 120

Qy         90 LeuLeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyrAsp 109
              |||                :::|||||||:::   ||||||   ||||||||||||||||
Db        121 CTGGAGAAACGCCATTCTCTGGAATACAGCCTCCGAATCCAGAAGGTGGATGTCTATGAT 180

Qy        110 GluGlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHis 129
              ||||||   ||||||||||||||||||||   :::   ||||||||||||:::|||:::
Db        181 GAGGGTTCCTACACTTGCTCAGTTCAGACACAGCATGAGCCCAAGACCTCCCAAGTTTAC 240

Qy        130 LeuIleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGlu 149
              ||||||||||||||   |||||||||       ||||||||||:::::::::||||||
Db        241 TTGATCGTACAAGTCCCACCAAAGATCTCCAATATCTCCTCGGATGTCACTGTGAATGAG 300

Qy        150 GlyAsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrp 169
              |||:::|||:::::|||   |||:::|||   ||||||||||||||   :::||||||
Db        301 GGCAGCAACGTGACTCTGGTCTGCATGGCCAATGGCCGTCCTGAACCTGTTATCACCTGG 360

Qy        170 ArgHisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGln 189
              ||||||:::::|||           |||      |||:::||||||||||||||||
Db        361 AGACACCTTACACCAACTGGAAGGGAATTTGAAGGAGAAGAAGAATATCTGGAGATCCTT 420

Qy        190 GlyIleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAla 209
              ||||||||||||||||||||||   |||||||||   |||:::|||:::|||::::::
Db        421 GGCATCACCAGGGAGCAGTCAGGCAAATATGAGTGCAAAGCTGCCAACGAGGTCTCCTCG 480

Qy        210 ProValValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAlaLys 229
                    |||:::::::|||||||||||||||||||||||||||||   |||:::|||:::|||
Db        481 GCGGATGTCAAACAAGTCAAGGTCACTGTGAACTATCCTCCCACTATCACAGAATCCAAG 540

Qy        230 GlyThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValPro 249
                             |||:::::::   :::|||:::|||||||||||||||||||||||
Db        541 AGCAATGAAGCCACCACAGGACGACAAGCTTCACTCAAATGTGAGGCCTCGGCAGTGCCT 600

Qy        250 SerAlaGluPheGlnTrpTyrLysAspAspLysArgLeuIleGluGlyLysLysGlyVal 269
              :::   :::|||:::||||||:::||||||   |||   |||           |||:::
Db        601 GCACCTGACTTTGAGTGGTACCGGGATGACACTAGG---ATAAATAGTGCCAATGGCCTT 657

Qy        270 LysValGluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAsp 289
              ::::::::::::            |||   |||          ||||||:::|||
Db        658 GAGATTAAGAGCACGGAGGGCCAGTCTTCCCTGACGGTGACCAACGTCACTGAGGAGCAC 717

Qy        290 TyrGlyAsnTyrThrCysValAlaSerAsnLysLeuGly 302
              |||||||||||||||||||||:::|||||||||||||
Db        718 TACGGCAACTACACCTGTGTGGCTGCCAACAAGCTGGGG 756
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```
RESULT 13
US-08-414-657D-18
; Sequence 18, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  756 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...756
;      OTHER INFORMATION:
US-08-414-657D-18

Alignment Scores:
Pred. No.:              6.67e-84        Length:         756
Score:                  795.50          Matches:        144
Percent Similarity:     76.68%          Conservative:   50
Best Local Similarity:  56.92%          Mismatches:     58
Query Match:            44.05%          Indels:         1
DB:                     2               Gaps:           1

US-10-017-084A-523 (1-344) x US-08-414-657D-18 (1-756)

Qy         50 GlyGluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeu 69
              |||:::::::|||   |||||||||   ::::::::::::   ::::::|||||||||||||
Db          1 GGGGACACGGCCATCCTCAGGTGTGTGGTAGAAGACAAGAACTCGAAAGTGGCCTGGTTG 60

Qy         70 AsnArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgValVal 89
              |||||||||   |||:::::::||||||:::|||||||||   |||||||||||||||
Db         61 AACCGCTCTGGCATCATCTTCGCTGGACACGACAAGTGGTCTCTGGACCCTCGGGTTGAG 120

Qy         90 LeuLeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyrAsp 109
              |||                 :::|||||:::   ||||||   ||||||||||||||||
Db        121 CTGGAGAAACGCCATGCTCTGGAATACAGCCTCCGAATCCAGAAGGTGGATGTCTATGAT 180

Qy        110 GluGlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHis 129
              ||||||   |||||||||||||||||||   :::   |||||||||||:::|||:::
Db        181 GAAGGATCCTACACATGCTCAGTTCAGACACAGCATGAGCCCAAGACCTCTCAAGTTTAC 240

Qy        130 LeuIleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGlu 149
              ||||||||||||||   |||||||||      ||||||||||||:::::::::|||||
Db        241 TTGATTGTACAAGTTCCACCAAAGATCTCCAACATCTCCTCGGATGTCACTGTGAATGAG 300

Qy        150 GlyAsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrp 169
              |||:::|||:::::::|||   |||:::|||   ||||||||||||||   :::||||||
Db        301 GGCAGCAATGTAACCCTGGTCTGCATGGCCAATGGGCGCCCTGAACCTGTTATCACCTGG 360

Qy        170 ArgHisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGln 189
              ||||||:::::|||              |||      |||:::|||||||||||||||||
Db        361 AGACACCTTACACCACTTGGAAGAGAATTTGAAGGAGAAGAAGAATATCTGGAGATCCTA 420

Qy        190 GlyIleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAla 209
              ||||||||||||||||||||||   |||||||||   |||:::|||:::|||::::::
Db        421 GGCATCACCAGGGAACAGTCAGGCAAATATGAGTGCAAGGCTGCCAACGAGGTCTCCTCC 480

Qy        210 ProValValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAlaLys 229
                    |||::::::|||||||||||||||||||||||||||||   |||:::|||:::|||
Db        481 GCGGATGTCAAACAAGTCAAGGTCACTGTGAACTATCCACCCACCATCACAGAGTCTAAG 540

Qy        230 GlyThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValPro 249
                               |||:::::::   :::|||:::|||||||||||||||||||||
Db        541 AGCAATGAAGCCACCACAGGACGACAAGCTTCCCTCAAATGTGAAGCCTCAGCGGTGCCT 600

Qy        250 SerAlaGluPheGlnTrpTyrLysAspAspLysArgLeuIleGluGlyLysLysGlyVal 269
              :::   :::|||:::|||||:::||||||   |||   |||          |||:::
Db        601 GCACCTGACTTTGAGTGGTACCGGGATGACACCAGG---ATAAACAGTGCAAACGGCCTT 657

Qy        270 LysValGluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAsp 289
              ::::::::::::             |||   |||         ||||||:::|||
Db        658 GAGATTAAGAGCACTGAGGGCCAGTCCTCCCTGACGGTGACCAACGTCACTGAGGAACAC 717

Qy        290 TyrGlyAsnTyrThrCysValAlaSerAsnLysLeuGly 302
              ||||||||||||||||||||||||:::|||||||||||||
Db        718 TACGGCAACTATACCTGTGTGGCTGCCAACAAGCTCGGC 756

RESULT 14
US-09-484-970B-66
; Sequence 66, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
;  APPLICANT:  Jones, Karen A.
;  APPLICANT:  Volkmuth, Wayne
;  APPLICANT:  Walker, Michael G.
;  TITLE OF INVENTION:  BONE REMODELING GENES
;  FILE REFERENCE:  PB-0014 US
;  CURRENT APPLICATION NUMBER: US/09/484,970B
;  CURRENT FILING DATE:  2000-01-18
;  NUMBER OF SEQ ID NOS:  172
;  SOFTWARE:  PERL Program
; SEQ ID NO 66
;   LENGTH: 6814
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6426186 199882.3
;   NAME/KEY: unsure
;   LOCATION: 1838, 5528
;   OTHER INFORMATION: a, t, c, g, or other
US-09-484-970B-66

Alignment Scores:
Pred. No.:              5.39e-20        Length:         6814
Score:                  263.50          Matches:        92
Percent Similarity:     38.39%          Conservative:   32
Best Local Similarity:  28.48%          Mismatches:     148
Query Match:            14.59%          Indels:         51
DB:                     4               Gaps:           13
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US-10-017-084A-523 (1-344) x US-09-484-970B-66 (1-6814)

Qy          8 MetHisAsnSerIleSerTrpAlaIlePheThrGlyLeuAlaAlaLeuCysLeuPheGln 27
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Db       1006 ATGGCAAAGAACGTGGCCGGAGAGGTGAAGACGCAAGAGGTGACCCTCAGGTACTTC--- 1062

Qy         28 GlyValProValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrVal 47
              |||   |||   |||          ||||||          |||       |||
Db       1063 GGGTCTCCAGCTCGA---------CCCACTTTTGTAATCCAGCCACAGAATACAGAGGTG 1113

Qy         48 ArgGlnGlyGluSerAlaThrLeuArgCysThrIleAspAsnArg---ValThrArgVal 66
                 |||||||||   ||||||   |||:::                  |||:::
Db       1114 CTGGTTGGGGAGAGCGTCACGCTGGAGTGCAGCGCCACAGGCCACCCCCCGCCGCGGATC 1173

Qy         67 AlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeu------ 84
              :::|||                                  |||:::      |||
Db       1174 TCCTGGACGAGA----------------------GGTGACCGCACACCCTTGCCAGTT 1209

Qy         85 AspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsn 104
              ||||||||||||           |||                 :::   |||||||||
Db       1210 GACCCGCGGGTG-----------AACATCACGCCTTCTGGCGGGCTTTACATACAGAAC 1257

Qy        105 ValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAspAsnHisProLys 124
              |||      |||   |||   |||   ||||||        :::
Db       1258 GTCGTACAGGGGGACAGCGGAGAGTATGCGTGCTCTGCGACCAACAACATTGACAGCGTC 1317

Qy        125 ThrSerArgValHisLeuIleValGlnValSerProLysIleValGluIleSerSerAsp 144
              :::        :::||||||||||      |||:::                  |||
Db       1318 CATGCCACCGCTTTCATCATCGTCCAGGCTCTTCCTCAGTTCACTGTGACGCCTCAGGAC 1377

Qy        145 IleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGlu 164
              :::   ||||||      :::         |||   |||   |||   |||
Db       1378 AGAGTCGTTATTGAGGGCCAGACCGTGGATTTCCAGTGTGAAGCCAAGGGCAACCCGCCG 1437

Qy        165 ProThrValThrTrp--------------------------------ArgHisIleSer 173
              |||   :::   |||                               ||||||:::
Db       1438 CCCGTCATCGCCTGGACCAAGGGAGGGAGCCAGCTCTCCGTGGACCGGCGGCACCTG--- 1494

Qy        174 ProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArg 193
                          |||                 |||   |||   |||:::
Db       1495 -----------------GTCCTGTCATCGGGAACACTTAGAATCTCTGGTGTTGCCCTC 1536

Qy        194 GluGlnSerGlyAspTyrGluCysSerAla----------------SerAsnAspValAla 208
                 |||  ||||||||||   |||                  |||      |||
Db       1537 CACGACCAGGGCCAGTACGAATGCCAGGCTGTCAACATCATCGGCTCCCAGAAGGTCGTG 1596

Qy        209 AlaProValValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAla 228
              |||   :::      :::   :::||||||          |||  :::   |||
Db       1597 GCCCACCTGACTGTGCAGCCCAGAGTCACC---------CCAGTGTTTGCCAGCATTCCC 1647

Qy        229 LysGlyThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaVal 248
                 |||   |||   ||||||              |||   |||   :::
Db       1648 AGCGACACAACAGTGGAGGTGGGCGCCAATGTGCAGCTCCCGTGCAGCTCCCAGGGCGAG 1707

Qy        249 ProSerAlaGluPheGlnTrpTyrLysAspAspLysArgLeuIleGlu---GlyLysLys 267
              |||          |||   ||||||      :::::  |||   ||||||
Db       1708 CCCGAGCCAGCCATCACCTGGAACAAGGATGGGGTTCAGGTGACAGAAAGTGGAAAATTT 1767

Qy        268 GlyValLysValGluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGlu 287
              :::      |||   |||   ||||||:::          :::|||      :::
Db       1768 CACATCAGCCCTGAAGGA------TTCTTGACC---------ATCAATGACGTTGGCCCT 1812

Qy        288 HisAspTyrGlyAsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSer 307
              |||   |||   |||   |||   |||   |||   :::|||      :::   |||
Db       1813 GCAGACGCAGGTCGCTATGAGTGTGNGGCCCGGAACACCATTGGGTCGGCCTCGGTGAGC 1872

Qy        308 IleMetLeu 310
              :::::::|||
Db       1873 ATGGTGCTC 1881

RESULT 15
US-08-659-984A-2
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; Sequence 2, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
;   APPLICANT: Anderson, John P.
;   APPLICANT: Sinha, Sukanto
;   APPLICANT: Jacobson-Croak, Kirsten L.
;   TITLE OF INVENTION: Assays for Detecting Beta-Secretase
;   TITLE OF INVENTION: Inhibition
;   NUMBER OF SEQUENCES: 21
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Townsend and Townsend and Crew LLP
;     STREET: Two Embarcadero Ctr., 8th Floor
;     CITY: San Francisco
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94111-3834
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/659,984A
;     FILING DATE: 07-JUN-1996
;     CLASSIFICATION: 436
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/485,152
;     FILING DATE: 07-JUN-1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Heslin, James M.
;     REGISTRATION NUMBER: 29,541
;     REFERENCE/DOCKET NUMBER: 15270-002810US
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 415-326-2400
;     TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1266 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
US-08-659-984A-2

Alignment Scores:
Pred. No.:              2.91e-20        Length:         1266
Score:                  256.00          Matches:        92
Percent Similarity:     42.44%          Conservative:   54
Best Local Similarity:  26.74%          Mismatches:     126
Query Match:            14.17%          Indels:         72
DB:                     2               Gaps:           16

US-10-017-084A-523 (1-344) x US-08-659-984A-2 (1-1266)

Qy         31 ValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArgGlnGly 50
              |||:::          ||||||          ||||||||||||   :::|||
Db         13 GTTAAAGGCAGCCAAGGGCAGTTTCCA---CTAACACAGAATGTAACCGTTGTTGAAGGT 69

Qy         51 GluSerAlaThrLeuArgCysThrIleAsp---AsnArgValThrArgValAlaTrpLeu 69
                 :::|||  |||   |||   :::|||   |||       |||   :::   |||
Db         70 GGAACTGCAATTTTGACCTGCAGGGTTGATCAAAATGATAACACCTCCCTCCAGTGGTCA 129

Qy         70 Asn---ArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgVal 88
              |||          ||||||      :::   |||         |||   |||:::
Db        130 AATCCAGCTCAACAGACTCTGTACTTTGACGACAAGAAAGCTTTAAGGGACAATAGGATC 189

Qy         89 ValLeuLeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyr 108
                 |||:::      :::      :::   ||||||   :::   :::|||   :::
Db        190 GAGCTGGTTCGCGCTTCCTGGCATGAATTGAGTATTAGTGTCAGTGATGTGTCTCTCTCT 249

Qy        109 AspGluGlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgVal 128
              |||||||||  ||||||||||||:::  |||                |||||||||:::
Db        250 GATGAAGGACAGTACACCTGTTCTTTATTTACA---ATGCCTGTCAAAACTTCCAAGGCA 306
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Qy        129 HisLeuIleValGlnValSerProLysIleValGluIleSerSerAspIleSer---Ile 147
              :::|||   |||       |||:::     :::||||||         |||   :::
Db        307 TATCTCACCGTTCTGGGTGTTCCTGAAAAGCCTCAGATTAGTGGATTCTCATCACCAGTT 366

Qy        148 AsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThrGly---ArgProGluProThr 166
              ||||||:::   :::   ||||||||     :::|||   :::|||
Db        367 ATGGAGGGTGACTTGATGCAGCTGACTTGCAAAACATCTGGTAGTAAACCTGCAGCTGAT 426

Qy        167 ValThrTrpArgHisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeu 186
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Db        427 ATAAGATGG-------------------------TTCAAAAATGACAAAGAGATTAAA 459

Qy        187 GluIleGlnGlyIleThrArgGluGlnSerGly-------------------------- 197
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Qy        198 ---AspTyrGluCysSerAlaSerAsnAsp---------------------------- 206
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Db        520 CTGGACTTCCGAGTGGACCGGAGTGATGATGGAGTGGCGGTCATCTGCAGAGTAGATCAC 579

Qy        207 ---------ValAlaAlaProValValArgArgValLysValThrValAsnTyrProPro 223
                      |||   |||   |||           :::   ::::::|||   |||
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Qy        224 TyrIleSerGluAlaLysGlyThrGlyValPro---ValGlyGlnLysGlyThrLeuGln 242
              :::               |||      |||      ||||||         |||
Db        640 TCAGTTAAGATTATACCATCGACTCCTTTTCCACAAGAAGGACAGCCTTTAATTTTGACT 699

Qy        243 CysGluAlaSerAlaValProSerAlaGlu---PheGlnTrpTyrLysAsp--------- 258
              |||||||:::        |||      |||          |||   ||||||
Db        700 TGTGAATCCAAAGGAAAACCACTGCCAGAACCTGTTTTGTGGACAAAGGATGGCGGAGAA 759

Qy        259 ------------AspLysArgLeuIleGluGlyLysLysGlyValLysValGluAsnArg 274
                         |||:::   ::::::   |||::::::
Db        760 TTACCAGATCCTGACCGAATGGTTGTGAGTGGTAGGGAG---------------------- 798

Qy        275 ProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThr 294
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Db        799 ---------CTAAACATTCTTTTCCTGAAC------AAAACGGATAATGGTACATATCGA 843

Qy        295 CysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGly 314
              |||   |||:::|||   :::|||   :::::::|||      :::|||
Db        844 TGTGAAGCCACAAACACCATTGGCCAAAGCAGTGCGGAATATGTTCTCATT--------- 894

Qy        315 AlaValSerGluValSerAsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuPro 334
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Db        895 ---GTGCATGATGTTCCCAAC-------------------------ACTTTGCTTCCC 924

Qy        335 LeuLeuValLeu 338
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Job time : 108 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 11, 2003, 04:30:41 ; Search time 1457 Seconds
(without alignments)
573.197 Million cell updates/sec

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Perfect score: 1806
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 1632420 seqs, 1213878141 residues

Total number of hits satisfying chosen parameters: 3264840

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
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-MAXLEN=2000000000 -USER=US10017084_@CGN_1_1_107_@runat_09092003_141327_21929
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1806	100.0	1679	10	US-09-978-697-522	Sequence 522, App
3	1806	100.0	1679	10	US-09-978-192A-522	Sequence 522, App
4	1806	100.0	1679	10	US-09-999-832A-522	Sequence 522, App
5	1806	100.0	1679	11	US-09-978-189-522	Sequence 522, App
6	1806	100.0	1679	11	US-09-978-608A-522	Sequence 522, App
7	1806	100.0	1679	11	US-09-978-585A-522	Sequence 522, App
8	1806	100.0	1679	11	US-09-978-191A-522	Sequence 522, App
9	1806	100.0	1679	11	US-09-978-403A-522	Sequence 522, App
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14	1806	100.0	1679	11	US-09-918-585A-522	Sequence 522, App
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21	1806	100.0	1679	12	US-09-978-375A-522	Sequence 522, App
22	1806	100.0	1679	12	US-09-978-188A-522	Sequence 522, App
23	1806	100.0	1679	12	US-09-978-298A-522	Sequence 522, App
24	1806	100.0	1679	12	US-10-137-870-375	Sequence 375, App
25	1806	100.0	1679	12	US-10-140-018-375	Sequence 375, App
26	1806	100.0	1679	12	US-10-140-021-375	Sequence 375, App
27	1806	100.0	1679	12	US-10-140-274-375	Sequence 375, App
28	1806	100.0	1679	12	US-10-140-471-375	Sequence 375, App
29	1806	100.0	1679	12	US-10-140-807-375	Sequence 375, App
30	1806	100.0	1679	12	US-10-140-922-375	Sequence 375, App
31	1806	100.0	1679	12	US-10-140-924-375	Sequence 375, App
32	1806	100.0	1679	12	US-10-140-926-375	Sequence 375, App
33	1806	100.0	1679	12	US-10-141-698-375	Sequence 375, App
34	1806	100.0	1679	12	US-10-141-702-375	Sequence 375, App
35	1806	100.0	1679	12	US-10-141-704-375	Sequence 375, App
36	1806	100.0	1679	12	US-10-142-421-375	Sequence 375, App
37	1806	100.0	1679	12	US-10-142-432-375	Sequence 375, App
38	1806	100.0	1679	12	US-10-142-767-375	Sequence 375, App
39	1806	100.0	1679	12	US-10-143-031A-522	Sequence 522, App
40	1806	100.0	1679	12	US-10-143-033-375	Sequence 375, App
41	1806	100.0	1679	12	US-10-144-994-375	Sequence 375, App
42	1806	100.0	1679	12	US-10-145-628-375	Sequence 375, App
43	1806	100.0	1679	12	US-10-145-631-375	Sequence 375, App
44	1806	100.0	1679	12	US-10-145-633-375	Sequence 375, App
45	1806	100.0	1679	12	US-10-145-746-375	Sequence 375, App

ALIGNMENTS

RESULT 1
US-09-978-295A-522
; Sequence 522, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
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; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
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Alignment Scores:

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US-10-017-084A-523 (1-344) x US-09-978-295A-522 (1-1679)

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RESULT 2
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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C27
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;  PRIOR APPLICATION NUMBER: 60/085704
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
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Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              100.00%       Indels:          0
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US-10-017-084A-523 (1-344) x US-09-978-697-522 (1-1679)

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RESULT 3
US-09-978-192A-522
; Sequence 522, Application US/09978192A
; Patent No. US20020177553A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C9
;  CURRENT APPLICATION NUMBER: US/09/978,192A
;  CURRENT FILING DATE:  2001-10-15
;  PRIOR APPLICATION NUMBER: 09/918585
;  PRIOR FILING DATE: 2001-07-30
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;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/085697

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Query Match:            100.00%         Indels:          0
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US-10-017-084A-523 (1-344) x US-09-978-192A-522 (1-1679)

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RESULT 4
US-09-999-832A-522
; Sequence 522, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C63
;  CURRENT APPLICATION NUMBER: US/09/999,832A
;  CURRENT FILING DATE:  2001-10-24
;  PRIOR APPLICATION NUMBER: 09/918585
;  PRIOR FILING DATE: 2001-07-30
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
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Query Match:            100.00%       Indels:          0
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US-10-017-084A-523 (1-344) x US-09-999-832A-522 (1-1679)

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Qy         21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
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Db        194 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 253

Qy         41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        254 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 313

Qy         61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        314 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 373

Qy         81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
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Db        374 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 433

Qy        101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493

Qy        121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
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Db        494 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 553

Qy        141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
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Db        554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613

Qy        161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673

Qy        181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy        201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy        221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853

Qy        241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        854 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 913

Qy        261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
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Db        914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 973

Qy        281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

Qy        301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1093

Qy        321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1153

Qy        341 LeuLeuLysPhe 344
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Db       1154 CTTCTCAAATTT 1165

RESULT 5
US-09-978-189-522
; Sequence 522, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C7
;  CURRENT APPLICATION NUMBER: US/09/978,189
;  CURRENT FILING DATE:  2001-10-15
;  PRIOR APPLICATION NUMBER: 09/918585
;  PRIOR FILING DATE: 2001-07-30
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/064249
;  PRIOR FILING DATE: 1997-11-03
;  PRIOR APPLICATION NUMBER: 60/065311
;  PRIOR FILING DATE: 1997-11-13
;  PRIOR APPLICATION NUMBER: 60/066364
;  PRIOR FILING DATE: 1997-11-21
;  PRIOR APPLICATION NUMBER: 60/077450
;  PRIOR FILING DATE: 1998-03-10
;  PRIOR APPLICATION NUMBER: 60/077632
;  PRIOR FILING DATE: 1998-03-11
;  PRIOR APPLICATION NUMBER: 60/077641
;  PRIOR FILING DATE: 1998-03-11
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; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
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; PRIOR FILING DATE: 1998-03-13
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; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
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; PRIOR FILING DATE: 1998-05-07
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; PRIOR FILING DATE: 1998-05-15
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; PRIOR APPLICATION NUMBER: 60/085579
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; PRIOR FILING DATE: 1998-05-15

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;  PRIOR APPLICATION NUMBER: 60/085704
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
Pred. No.:              9.94e-216       Length:         1679
Score:                  1806.00         Matches:        344
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     11              Gaps:           0

US-10-017-084A-523 (1-344) x US-09-978-189-522 (1-1679)

Qy          1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
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Db        134 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 193

Qy         21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        194 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 253

Qy         41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
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Db        254 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 313

Qy         61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
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Db        314 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 373

Qy         81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
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Db        374 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 433

Qy        101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
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Db        434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493

Qy        121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
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Db        494 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 553

Qy        141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
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Db        554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613

Qy        161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
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Db        614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673

Qy        181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy        201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy        221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
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Db        794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853

Qy        241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
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Db        854 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 913

Qy        261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 973

Qy        281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

Qy        301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
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Qy        321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
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Qy        341 LeuLeuLysPhe 344
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Db       1154 CTTCTCAAATTT 1165

RESULT 6
US-09-978-608A-522
; Sequence 522, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C22
;  CURRENT APPLICATION NUMBER: US/09/978,608A
;  CURRENT FILING DATE:  2001-10-16
;  NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 522
;   LENGTH: 1679
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-978-608A-522

Alignment Scores:
Pred. No.:              9.94e-216       Length:         1679
Score:                  1806.00         Matches:        344
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     11              Gaps:           0

US-10-017-084A-523 (1-344) x US-09-978-608A-522 (1-1679)

Qy          1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 193

Qy         21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
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Db        194 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 253

Cy         41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
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Db        314 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 373

Qy         81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
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Qy        101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
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Db        434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493

Qy        121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
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Qy        141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
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Db        554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613

Qy        161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673

Qy        181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy        201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy        221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853

Qy        241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        854 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 913

Qy        261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 973

Qy        281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

Qy        301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1093

Qy        321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1153

Qy        341 LeuLeuLysPhe 344
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Db       1154 CTTCTCAAATTT 1165

RESULT 7
US-09-978-585A-522
; Sequence 522, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT: Baker Kevin P.
;  APPLICANT: Botstein, David
;  APPLICANT: Desnoyers, Luc
;  APPLICANT: Eaton, Dan
;  APPLICANT: Ferrara, Napoleon
;  APPLICANT: Filvaroff, Ellen
;  APPLICANT: Fong, Sherman
;  APPLICANT: Gao, Wei-Qiang
;  APPLICANT: Gerber, Hanspeter
;  APPLICANT: Gerritsen, Mary E.
;  APPLICANT: Goddard, Audrey
;  APPLICANT: Godowski, Paul J.
;  APPLICANT: Grimaldi, J. Christopher
;  APPLICANT: Gurney, Austin L.
;  APPLICANT: Hillan, Kenneth J
;  APPLICANT: Kljavin, Ivar J.
;  APPLICANT: Kuo, Sophia S.
;  APPLICANT: Napier, Mary A.
;  APPLICANT: Pan, James
;  APPLICANT: Paoni, Nicholas F.
;  APPLICANT: Roy, Margaret Ann
;  APPLICANT: Shelton, David L.
;  APPLICANT: Stewart, Timothy A.
;  APPLICANT: Tumas, Daniel
;  APPLICANT: Williams, P. Mickey
;  APPLICANT: Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C15
;  CURRENT APPLICATION NUMBER: US/09/978,585A
;  CURRENT FILING DATE:  2001-10-16
;  NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 522
;   LENGTH: 1679
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-978-585A-522

Alignment Scores:
Pred. No.:                9.94e-216       Length:          1679
Score:                    1806.00         Matches:         344
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       11              Gaps:            0

US-10-017-084A-523 (1-344) x US-09-978-585A-522 (1-1679)

Qy          1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 193

Qy         21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        194 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 253

Qy         41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        254 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 313

Qy         61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        314 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 373

Qy         81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 433

Qy        101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493
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Qy        121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
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Db        494 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 553

Qy        141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
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Db        554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613

Qy        161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673

Qy        181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy        201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy        221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853

Qy        241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        854 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 913

Qy        261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 973

Qy        281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

Qy        301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
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Db       1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1093

Qy        321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
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Db       1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1153

Qy        341 LeuLeuLysPhe 344
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Db       1154 CTTCTCAAATTT 1165

RESULT 8
US-09-978-191A-522
; Sequence 522, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C4
;  CURRENT APPLICATION NUMBER: US/09/978,191A
;  CURRENT FILING DATE:  2001-10-15
;  PRIOR APPLICATION NUMBER: 09/918585
;  PRIOR FILING DATE: 2001-07-30
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/064249
;  PRIOR FILING DATE: 1997-11-03
;  PRIOR APPLICATION NUMBER: 60/065311
;  PRIOR FILING DATE: 1997-11-13
;  PRIOR APPLICATION NUMBER: 60/066364
;  PRIOR FILING DATE: 1997-11-21
;  PRIOR APPLICATION NUMBER: 60/077450
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;  PRIOR APPLICATION NUMBER: 60/080333
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; PRIOR FILING DATE: 1998-04-01
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; PRIOR FILING DATE: 1998-04-01
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; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
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; PRIOR APPLICATION NUMBER: 60/085689
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; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.:	9.94e-216	Length:	1679
Score:	1806.00	Matches:	344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	11	Gaps:	0

US-10-017-084A-523 (1-344) x US-09-978-191A-522 (1-1679)

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Qy          1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 193

Qy         21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        194 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 253

Qy         41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
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Db        254 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 313

Qy         61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        314 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 373

Qy         81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 433

Qy        101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
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Db        434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493

Qy        121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        494 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 553

Qy        141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
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Db        554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613
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Qy        161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673

Qy        181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy        201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy        221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGACA 853

Qy        241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        854 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 913

Qy        261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
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Db        914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 973

Qy        281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
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Db        974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

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Qy        321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
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Qy        341 LeuLeuLysPhe 344
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RESULT 9
US-09-978-403A-522
; Sequence 522, Application US/09978403A
; Publication No. US20030050240A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C17
;  CURRENT APPLICATION NUMBER: US/09/978,403A
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; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.:	9.94e-216	Length:	1679
Score:	1806.00	Matches:	344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	11	Gaps:	0

US-10-017-084A-523 (1-344) x US-09-978-403A-522 (1-1679)

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Qy          1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
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Db        134 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 193

Qy         21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
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Db        314 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 373

Qy         81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
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Qy        101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
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Qy        121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
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Qy        141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
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Db        614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673

Qy        181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
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RESULT 10
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; Publication No. US20030050241A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C25
;  CURRENT APPLICATION NUMBER: US/09/978,564A
;  CURRENT FILING DATE:  2001-10-16
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; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
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; PRIOR APPLICATION NUMBER: 60/085579
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; PRIOR APPLICATION NUMBER: 60/085573
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.:	9.94e-216	Length:	1679
Score:	1806.00	Matches:	344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	11	Gaps:	0

US-10-017-084A-523 (1-344) x US-09-978-564A-522 (1-1679)

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Qy          1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
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Db        134 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 193

Qy         21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
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Db        194 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 253

Qy         41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
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Db        254 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 313

Qy         61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
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Db        314 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 373

Qy         81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
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Qy        101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
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Qy        121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
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Qy        141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
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Qy        161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
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Db        614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673

Qy        181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
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Db        674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy        201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
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Db        734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy        221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
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Db        854 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 913

Qy        261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
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Db        914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 973

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Db        974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

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RESULT 11
US-09-999-833A-522
; Sequence 522, Application US/09999833A
; Publication No. US20030054405A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C65
;  CURRENT APPLICATION NUMBER: US/09/999,833A
;  CURRENT FILING DATE:  2001-10-24
;  PRIOR APPLICATION NUMBER: 09/918585
;  PRIOR FILING DATE: 2001-07-30
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/064249
;  PRIOR FILING DATE: 1997-11-03
;  PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.:	9.94e-216	Length:	1679
Score:	1806.00	Matches:	344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	11	Gaps:	0

US-10-017-084A-523 (1-344) x US-09-999-833A-522 (1-1679)

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Qy          1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
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Qy        181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
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Db        674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy        201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
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Db        794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853

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Db        854 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 913
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RESULT 12
US-09-981-915A-522
; Sequence 522, Application US/09981915A
; Publication No. US20030054986A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION:  Acids Encoding the Same
; FILE REFERENCE: P2630P1C12
; CURRENT APPLICATION NUMBER: US/09/981,915A
; CURRENT FILING DATE:  2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
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; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.:	9.94e-216	Length:	1679
Score:	1806.00	Matches:	344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	11	Gaps:	0

US-10-017-084A-523 (1-344) x US-09-981-915A-522 (1-1679)

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; Publication No. US20030055216A1
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;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C14
;  CURRENT APPLICATION NUMBER: US/09/978,824
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; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
Pred. No.: 9.94e-216 Length: 1679
Score: 1806.00 Matches: 344

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-10-017-084A-523 (1-344) x US-09-978-824-522 (1-1679)

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Qy      201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
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Db      734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy      221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
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Qy      261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
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Db      914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 973

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RESULT 14
US-09-918-585A-522
; Sequence 522, Application US/09918585A
; Publication No. US20030060406A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C1
;  CURRENT APPLICATION NUMBER: US/09/918,585A
;  CURRENT FILING DATE:  2001-07-30
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; PRIOR APPLICATION NUMBER: 60/086023

Alignment Scores:

Pred. No.:	9.94e-216	Length:	1679
Score:	1806.00	Matches:	344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	11	Gaps:	0

US-10-017-084A-523 (1-344) x US-09-918-585A-522 (1-1679)

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Qy        1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
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Db      674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

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RESULT 15

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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C21
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; CURRENT FILING DATE: 2002-05-16
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;  PRIOR APPLICATION NUMBER: 60/084639
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;  PRIOR APPLICATION NUMBER: 60/084640
;  PRIOR FILING DATE: 1998-05-07
;  PRIOR APPLICATION NUMBER: 60/084598
;  PRIOR FILING DATE: 1998-05-07
;  PRIOR APPLICATION NUMBER: 60/084600
;  PRIOR FILING DATE: 1998-05-07
;  PRIOR APPLICATION NUMBER: 60/084627
;  PRIOR FILING DATE: 1998-05-07
;  PRIOR APPLICATION NUMBER: 60/084643
;  PRIOR FILING DATE: 1998-05-07
;  PRIOR APPLICATION NUMBER: 60/085339
;  PRIOR FILING DATE: 1998-05-13
;  PRIOR APPLICATION NUMBER: 60/085338
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;  PRIOR APPLICATION NUMBER: 60/085323
;  PRIOR FILING DATE: 1998-05-13
;  PRIOR APPLICATION NUMBER: 60/085582
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/085700
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/085689
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/085579
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;  PRIOR APPLICATION NUMBER: 60/085580
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;  PRIOR APPLICATION NUMBER: 60/085573
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/085704
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
Pred. No.:              9.94e-216       Length:         1679
Score:                  1806.00         Matches:        344
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
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US-10-017-084A-523 (1-344) x US-09-978-423A-522 (1-1679)

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Qy         41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
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Qy        101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
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Qy        141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
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Qy        181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
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Qy        201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
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Db        734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy        221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
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Db        854 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 913

Qy        261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
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Db        914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 973

Qy        281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
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Db        974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

Qy        301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
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Qy        321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
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Db       1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1153

Qy        341 LeuLeuLysPhe 344
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Db       1154 CTTCTCAAATTT 1165

Search completed: September 11, 2003, 05:38:57
Job time : 1482 secs
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GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 11, 2003, 03:07:39 ; Search time 2500 Seconds
(without alignments)
3344.296 Million cell updates/sec

Title: US-10-017-084A-523
Perfect score: 1806
Sequence: 1 MKTIQPKMHNSISWAIFTGL.....RRAGCVWLLPLLVLHLLLKF 344

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool_p/US10017084/runat_09092003_141326_21883/app_query.fasta_1.519
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
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23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1780	98.6	1808	11	AK045973	AK045973 Mus muscu
2	1780	98.6	1808	11	AK046377	AK046377 Mus muscu
3	1254	69.4	765	14	CD354474	CD354474 UI-M-GM0-
4	1199.5	66.4	856	13	BU155617	BU155617 AGENCOURT
5	1167	64.6	1039	10	BE798585	BE798585 601581610
6	1112	61.6	890	14	CD327172	CD327172 AGENCOURT
7	1062.5	58.8	1085	9	AL533026	AL533026 AL533026
8	1047	58.0	740	13	BU368328	BU368328 603789424
9	1042	57.7	840	13	BU320256	BU320256 603851118
10	1005.5	55.7	849	12	BI755360	BI755360 603024964
11	982.5	54.4	865	12	BI666583	BI666583 603291469
12	973	53.9	601	14	CB582386	CB582386 AMGNNUC:N
13	929	51.4	793	13	BU365385	BU365385 603786031
14	926	51.3	545	10	BE263639	BE263639 601192064
15	925.5	51.2	979	10	BG261691	BG261691 602373361
16	916.5	50.7	2768	11	AK030681	AK030681 Mus muscu
17	912	50.5	732	12	BI551784	BI551784 603197479
18	910	50.4	553	10	BE864555	BE864555 UI-M-BH1-
19	907	50.2	524	10	BE014142	BE014142 125737 MA
c 20	902.5	50.0	859	14	CD325278	CD325278 AGENCOURT
21	894	49.5	2467	11	AK044845	AK044845 Mus muscu
22	890	49.3	784	12	BI549918	BI549918 603194765
23	881	48.8	768	9	AU080629	AU080629 AU080629
24	875	48.4	754	12	BI550038	BI550038 603192502
25	869	48.1	580	12	BI548566	BI548566 603189502
26	862.5	47.8	661	12	BM009450	BM009450 603629962
27	862.5	47.8	953	12	BM423716	BM423716 AGENCOURT
28	858.5	47.5	1033	12	BM807426	BM807426 AGENCOURT
29	855.5	47.4	1083	12	BM809227	BM809227 AGENCOURT
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31	818	45.3	728	14	CD353574	CD353574 UI-M-GM0-
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33	811.5	44.9	557	12	BM256660	BM256660 520043 MA
34	805	44.6	2096	11	AK035218	AK035218 Mus muscu
35	801	44.4	705	10	BG704152	BG704152 602687364
36	799	44.2	1953	11	AK030503	AK030503 Mus muscu
37	795	44.0	660	14	BY723873	BY723873 BY723873
38	791.5	43.8	764	12	BM945665	BM945665 UI-M-EM0-
39	772.5	42.8	849	14	CA472810	CA472810 AGENCOURT
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41	770	42.6	671	10	BB644996	BB644996 BB644996
c 42	761.5	42.2	858	14	CD325821	CD325821 AGENCOURT
43	761	42.1	663	12	BM724307	BM724307 UI-E-EO1-
44	759	42.0	2534	11	AK039193	AK039193 Mus muscu
c 45	742	41.1	827	14	CA306798	CA306798 UI-H-FT1-

ALIGNMENTS

RESULT 1
AK045973
LOCUS AK045973 1808 bp mRNA linear HTC 05-DEC-2002
DEFINITION Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230328N06 product:NEUROTRIMIN PRECURSOR (GP65) homolog [Rattus norvegicus], full insert sequence.
ACCESSION AK045973
VERSION AK045973.1 GI:26337738
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
MEDLINE 21085660
PUBMED 11217851
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 1808)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
FEATURES Location/Qualifiers
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BASE COUNT 550 a 431 c 462 g 365 t
ORIGIN

Alignment Scores:

Pred. No.:	1.73e-192	Length:	1808
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Percent Similarity:	99.42%	Conservative:	5
Best Local Similarity:	97.97%	Mismatches:	2
Query Match:	98.56%	Indels:	0
DB:	11	Gaps:	0

US-10-017-084A-523 (1-344) x AK045973 (1-1808)

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Qy          1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
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Db        204 ATGAAAACCATCCAGGCAAAAATGCACAATTCTATCTCGTGGGCAATCTTCACGGGGCTG 263

Qy         21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
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Qy        121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
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Db        564 AACCACCCTAAGACCTCCAGGGTCCACCTCATTGTACAAGTATCTCCCAAAATTGTAGAG 623

Qy        141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
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Db        624 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAACATCAGCCTCACTTGCATAGCCACA 683

Qy        161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
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Db        684 GGTAGACCGGAGCCTACAGTAACCTGGAGACATATTTCTCCCAAGGCCGTTGGCTTTGTG 743

Qy        181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        744 AGTGAGGATGAGTACCTGGAGATCCAGGGCATCACTCGGGAACAGTCAGGCGAGTACGAG 803

Qy        201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
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Db        804 TGCAGCGCCTCCAACGACGTGGCGGCACCAGTGGTACGAAGAGTGAAGGTCACCGTGAAC 863

Qy        221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        864 TATCCACCATACATCTCAGAAGCTAAGGGCACAGGTGTCCCCGTGGGGCAGAAGGGGACT 923

Qy        241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
              ||||||||||||||||||||||||||||||||||||||||||||:::||||||||||||||
Db        924 CTGCAGTGTGAAGCTTCCGCAGTCCCTTCAGCAGAATTTCAATGGTTCAAGGATGACAAA 983

Qy        261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
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Db        984 AGACTGGTCGAAGGAAAGAAGGGAGTCAAAGTGGAAAACAGACCTTTCCTTTCAAAACTC 1043

Qy        281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
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Db       1044 ACCTTTTTCAACGTCTCTGAACATGACTATGGGAACTACACATGTGTGGCCTCCAACAAG 1103

Qy        301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db       1104 CTGGGTCACACCAACGCCAGCATCATGCTATTTGGTCCCGGTGCTGTCAGTGAGGTCAAC 1163

Qy        321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
              ||||||||||||||||||||||||||:::|||||||||||||||||||||||||||||||
Db       1164 AATGGGACATCAAGGAGGGCAGGCTGCATTTGGCTCCTCCCTCTTCTGGTCTTACACCTG 1223

Qy        341 LeuLeuLysPhe 344
              ||||||||||||
Db       1224 CTCCTCAAATTT 1235

RESULT 2
AK046377
LOCUS       AK046377               1808 bp    mRNA    linear   HTC 05-DEC-2002
DEFINITION  Mus musculus adult male corpora quadrigemina cDNA, RIKEN
            full-length enriched library, clone:B230377K17 product:NEUROTRIMIN
            PRECURSOR (GP65) homolog [Rattus norvegicus], full insert sequence.
ACCESSION   AK046377
VERSION     AK046377.1  GI:26338018
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
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            Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
            Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
            Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
            Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
            Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
            Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
            Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6821), 685-690 (2001)
  MEDLINE   21085660
   PUBMED   11217851
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 1808)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
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            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
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            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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          Division of Experimental Animal Research in Riken contributed to
          prepare mouse tissues.
          Please visit our web site for further details.
          URL:http://genome.gsc.riken.go.jp/
          URL:http://fantom.gsc.riken.go.jp/..
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="FANTOM_DB:B230377K17"
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                     /clone="B230377K17"
                     /sex="male"
                     /tissue_type="corpora quadrigemina"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="adult"
     CDS             204. .1238
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                     (GP65) homolog [Rattus norvegicus] (SWISSPROT|Q62718,
                     evidence: FASTY, 99.4%ID, 92.1%length, match=951)
                     putative"
                     /codon_start=1
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                     QNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIAT
                     GRPEPTVTWRHISPKAVGFVSEDEYLEIQGITREQSGEYECSASNDVAAPVVRRVKVT
                     VNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWFKDDKRLVEGKKGVKVENRPF
                     LSKLTFFNVSEHDYGNYTCVASNKLGHTNASIMLFGPGAVSEVNNGTSRRAGCIWLLP
                     LLVLHLLLKF"
BASE COUNT      550 a    431 c    462 g    365 t
ORIGIN

Alignment Scores:
Pred. No.:              1.73e-192       Length:         1808
Score:                  1780.00         Matches:        337
Percent Similarity:     99.42%          Conservative:   5
Best Local Similarity:  97.97%          Mismatches:     2
Query Match:            98.56%          Indels:         0
DB:                     11              Gaps:           0

US-10-017-084A-523 (1-344) x AK046377 (1-1808)

Qy          1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db        204 ATGAAAACCATCCAGGCAAAAATGCACAATTCTATCTCGTGGGCAATCTTCACGGGGCTG 263

Qy         21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GCGGCTCTGTGCCTCTTCCAAGGAGTGCCGGTGCGTAGCGGAGATGCCACCTTTCCCAAA 323

Qy         41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 GCTATGGACAACGTGACGGTCAGGCAGGGGGAGAGCGCCACCCTCAGGTGCACAATTGAC 383

Qy         61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
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Db        384 AACCGAGTCACCCGGGTGGCCTGGCTAAACCGCAGTACCATCCTCTATGCTGGAAATGAC 443

Qy         81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
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Db        444 AAGTGGTGCCTAGATCCTCGTGTGGTCCTCCTGAGTAACACCCAGACCCAGTACAGCATT 503

Qy        101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
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Qy        121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
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Db        564 AACCACCCTAAGACCTCCAGGGTCCACCTCATTGTACAAGTATCTCCCAAAATTGTAGAG 623

Qy        141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
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Db        624 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAACATCAGCCTCACTTGCATAGCCACA 683

Qy        161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
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Qy        181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
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Db        744 AGTGAGGATGAGTACCTGGAGATCCAGGGCATCACTCGGGAACAGTCAGGCGAGTACGAG 803

Qy        201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
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Db        804 TGCAGCGCCTCCAACGACGTGGCGGCACCAGTGGTACGAAGAGTGAAGGTCACCGTGAAC 863

Qy        221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
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Qy        241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
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Qy        261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
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Db        984 AGACTGGTCGAAGGAAAGAAGGGAGTCAAAGTGGAAAACAGACCTTTCCTTTCAAAACTC 1043

Qy        281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
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Db       1044 ACCTTTTTCAACGTCTCTGAACATGACTATGGGAACTACACATGTGTGGCCTCCAACAAG 1103

Qy        301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
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Db       1104 CTGGGTCACACCAACGCCAGCATCATGCTATTTGGTCCCGGTGCTGTCAGTGAGGTCAAC 1163

Qy        321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
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Db       1164 AATGGGACATCAAGGAGGGCAGGCTGCATTTGGCTCCTCCCTCTTCTGGTCTTACACCTG 1223

Qy        341 LeuLeuLysPhe 344
              ||||||||||||
Db       1224 CTCCTCAAATTT 1235

RESULT 3
CD354474
LOCUS       CD354474                765 bp    mRNA    linear   EST 29-MAY-2003
DEFINITION  UI-M-GM0-cgd-g-16-0-UI.r1 NIH_BMAP_GM0 Mus musculus cDNA clone
            IMAGE: 30361215 5', mRNA sequence.
ACCESSION   CD354474
VERSION     CD354474.1  GI:31146975
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 765)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jim Lin, University of Iowa
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/mousef1.html
            This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
            Seq primer: pYX-5.
FEATURES             Location/Qualifiers
     source          1. .765
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/organism="Mus musculus"
/mol_type="mRNA"
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/db_xref="taxon:10090"
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/tissue_type="whole brain"
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/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I; Site_2: Not I; The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel.First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site.Double strand cDNA was size selected according to mRNA size fraction,ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGAACTGAAT. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

BASE COUNT 197 a 204 c 206 g 156 t 2 others
ORIGIN

Alignment Scores:

Pred. No.:	7.97e-133	Length:	765
Score:	1254.00	Matches:	246
Percent Similarity:	97.24%	Conservative:	1
Best Local Similarity:	96.85%	Mismatches:	6
Query Match:	69.44%	Indels:	2
DB:	14	Gaps:	1

US-10-017-084A-523 (1-344) x CD354474 (1-765)

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Qy          7 LysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeuAlaAlaLeuCysLeuPhe 26
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Qy         47 ValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgVal 66
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Db        125 GTCAGGCAGGGGGAGAGCGCCACCCTCAGGTGCACAATTGACAACCGAGTCACCCGGGTG 184

Qy         67 AlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspPro 86
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Db        185 GCCTGGCTAAACCGCAGTACCATCCTCTATGCTGGAAATGACAAGTGGTGCCTAGATCCT 244

Qy         87 ArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAsp 106
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Qy        107 ValTyrAspGluGlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSer 126
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Qy        127 ArgValHisLeuIleValGlnValSerProLysIleValGluIleSerSerAspIleSer 146
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Qy        147 IleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThr 166
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Qy        167 ValThrTrpArgHisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeu 186
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Db        485 GTAACCTGGAGACATATTTCTCCCAAGGCCGTTGGCTTTGTGAGTGAGGATGAGTACCTG 544
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```
Qy        187 GluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAsp 206
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Qy        207 ValAlaAlaProValValArgArgValLysValThrValAsnTyrProProTyrIleSer 226
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Db        605 GTGGCGGCACCAGTGGTACGAAGAGTGAAGGTCACCGTGAACTATCCACCATACATCTCA 664

Qy        227 GluAlaLysGlyThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSer 246
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Qy        247 AlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
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Db        725 CAGT--CCTTCAGCAGAATTTCATGGT---CNGGATGACAAA 761
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RESULT 4
BU155617
LOCUS BU155617 856 bp mRNA linear EST 03-SEP-2002
DEFINITION AGENCOURT_7973225 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6166839 5', mRNA sequence.
ACCESSION BU155617
VERSION BU155617.1 GI:22669149
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 856)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM13527 row: m column: 16
High quality sequence stop: 593.
FEATURES Location/Qualifiers
source 1..856
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6166839"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."
BASE COUNT 217 a 228 c 239 g 172 t
ORIGIN

Alignment Scores:

Pred. No.:	1.64e-126	Length:	856
Score:	1199.50	Matches:	243
Percent Similarity:	92.99%	Conservative:	9
Best Local Similarity:	89.67%	Mismatches:	13
Query Match:	66.42%	Indels:	7
DB:	13	Gaps:	3

US-10-017-084A-523 (1-344) x BU155617 (1-856)

```
Qy         11 SerIleSerTrpAlaIlePheThrGlyLeuAlaAlaLeuCysLeuPheGlnGlyValPro 30
              |||  ||||||:::    :::|||     :::|||           |||||||||
Db         48 AGTGCCTCGTGGTCGTGTCTCTCAGGCTGCTGTTCCTTG---TACCC-ACAGGAGTGCCC 103
```

```
Qy         31 ValArgSerGlyAspAlaThrProLysAlaMetAspAsnValThrValArgGlnGly 50
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        104 GTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGG 163

Qy         51 GluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsn 70
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        164 GAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAAC 223

Qy         71 ArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeu 90
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        224 CGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTT 283

Qy         91 LeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyrAspGlu 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        284 CTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAG 343

Qy        111 GlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeu 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        344 GGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTC 403

Qy        131 IleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGly 150
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        404 ATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGG 463

Qy        151 AsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArg 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        464 AACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGA 523

Qy        171 HisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGly 190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        524 CACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGC 583

Qy        191 IleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaPro 210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        584 ATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCC 643

Qy        211 ValValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGly 230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        644 GTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGT 703

Qy        231 ThrGlyVal-ProValGlyGlnLysGlyThrLeuGln-CysGluAlaSerAlaValProS 250
              |||||||| ||||||||||||||||||||||||||| |||||   ||||||||||||||
Db        704 ACAGGTGTCCCCCGTGGGACAAAAGGGGACACTGCAGTTGTGAAACCTCAGCAGTCCCCT 763

Qy        250 erAlaGlu-PheGlnTrpTyrLysAspAsp---LysArgLeuIleGluGlyLysLysGly 268
              |||||||| ||||||||||||||:::   |||     ::::::||||||||||||||
Db        764 CAGCAGAAATTCCAGTGGTACAGGGATGAACCAAAGACTGATTTGAAGGGAAAAAAAGGG 823

Qy        269 Val---LysValGluAsnArgProPhe 276
              |||   :::   :::|||   ||||||
Db        824 GTGGAAAGGGGGAAAAACGAACCTTTC 850

RESULT 5
BE798585
LOCUS       BE798585               1039 bp    mRNA    linear   EST 20-SEP-2000
DEFINITION  601581610F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935955 5',
            mRNA sequence.
ACCESSION   BE798585
VERSION     BE798585.1  GI:10219783
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1039)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM779  row: d  column: 04
            High quality sequence stop: 849.
FEATURES             Location/Qualifiers
     source          1. .1039
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3935955"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT      274 a    271 c    286 g    207 t      1 others
ORIGIN

Alignment Scores:
Pred. No.:                1.15e-122       Length:          1039
Score:                    1167.00         Matches:         243
Percent Similarity:       80.71%          Conservative:    8
Best Local Similarity:    78.14%          Mismatches:      24
Query Match:              64.62%          Indels:          37
DB:                       10              Gaps:            7

US-10-017-084A-523 (1-344) x BE798585 (1-1039)

Qy         56 ArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeu 75
              ||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db         66 AGGTGCACTATTGACAACCGGGTCGCCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTC 125

Qy         76 TyrAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGln 95
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 TATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAA 185

Qy         96 ThrGlnTyrSerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCys 115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 ACGCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGC 245

Qy        116 SerValGlnThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSer 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 TCGGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCT 305

Qy        136 ProLysIleValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeu 155
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 CCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTC 365

Qy        156 ThrCysIleAlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLys 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 ACCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAA 425

Qy        176 AlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGln 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAG 485

Qy        196 SerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgArgVal 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 TCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCCGTGGTACGGAGAGTA 545

Qy        216 LysValThrValAsnTyrProProTyrIleSerGluAlaLysGlyThrGlyValProVal 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTG 605

Qy        236 GlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrp 255
```

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 GGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGG 665

Qy        256 TyrLysAspAspLysArgLeuIleGluGly---LysLysGlyValLysValGluAsnArg 274
              ||||||||||||||||||||||||||||||      ::::||   ::::::|||||||||
Db        666 TACAAGGATGACAAAAGACTGATTGAAGGAACAGACAGGGGTGAACAGTTGGAAAACAGA 725

Qy        275 ProPheLeuSerLysLeuIlePhe------PheAsnValSer---GluHisAspTyr-Gl 291
              ||||||  |||     :::        |||||||||           |||||| ||
Db        726 CCTTTTCCTCCTCAAAAGTCATTCCTTCTTTCAATGTCCTCTGANCCATGGACTATGGG 785

Qy        291 yAsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAla-------------- 306
              ||||||||||||  |||     |||   ||||||||||||||||
Db        786 GAACTACACTTGCGGGGCTCCCA--AAAGCTGGGCACACCAATGCCAGATCATGCTATTG 843

Qy        307 ----------------------------------------------------------Se 307

Db        844 ACGTAAATAGAGAGCAGTAGAAAAGTTGGTACCAGTGGAGAGCCACAATGCCGGATAGGA 903

Qy        307 rIleMetLeuPheGlyProGlyAlaValSerGluValSerAsnGlyThrSerArg----- 325
              ::::::  |||   :::|||||||||                  |||
Db        904 CAGTCCAGTCTACAGCCCC---AGTGTGAGCGAGCCAAAGAAGAGCAGGGGCCGCGAGTG 960

Qy        326 ----------ArgAlaGly---CysValTrp 331
                       |||||||||   |||:::|||
Db        961 AGCAAGCTAGAGGGCGGGTTGGTGCCTCTGG 991

RESULT 6
CD327172
LOCUS       CD327172                890 bp    mRNA    linear   EST 28-MAY-2003
DEFINITION  AGENCOURT_14148239 NICHD_XGC_Eye1 Xenopus laevis cDNA clone
            IMAGE:6949575 5', mRNA sequence.
ACCESSION   CD327172
VERSION     CD327172.1  GI:31091503
KEYWORDS    EST.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus.
REFERENCE   1  (bases 1 to 890)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement:
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM14565  row: k  column: 14
            High quality sequence stop: 757.
FEATURES             Location/Qualifiers
     source          1. .890
                     /organism="Xenopus laevis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8355"
                     /clone="IMAGE:6949575"
                     /dev_stage="adult"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NICHD_XGC_Eye1"
                     /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 2.3 kb. Constructed by Life
                     Technologies. Note: This is a Xenopus Gene Collection (XGC
                     ) library."
BASE COUNT      226 a    214 c    240 g    210 t
```

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ORIGIN

Alignment Scores:
Pred. No.:              1.81e-116       Length:         890
Score:                  1112.00         Matches:        209
Percent Similarity:     88.93%          Conservative:   32
Best Local Similarity:  77.12%          Mismatches:     28
Query Match:            61.57%          Indels:         2
DB:                     14              Gaps:           0

US-10-017-084A-523 (1-344) x CD327172 (1-890)

Qy          4 IleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeuAlaAlaLeu 23
              :::|||   :::|||   :::|||:::   |||   |||||||:::|||||||||   |||
Db         69 CTGCAGGCAAGGATGCTGCACTCGGTTCCTTGGGTTATCTTCAGTGGGCTGGCTGTTCTT 128

Qy         24 CysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLysAlaMetAsp 43
              ||||||   ||||||||||||||||||||||||||||   ||||||||||||||||||
Db        129 TGCCTCCTGCAAGGAGTGCCGGTGCGCAGCGGGGATGCCGGCTTCCCTAAAGCCATGGAC 188

Qy         44 AsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAspAsnArgVal 63
              ||||||||||||||||||||:::||||||   ||||||||||||:::||||||||||||
Db        189 AACGTGACGGTTCGACAAGGGGACAGCGCCATCCTCAGGTGCACAGTAGACAACAGAGTG 248

Qy         64 ThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCys 83
              ||||||||||||||||||||||||||||||||||||||||||   ||||||||||||||
Db        249 ACACGAGTGGCCTGGCTAAATCGTAGTACCATCTTGTACACTGGCAATGACAAGTGGTCG 308

Qy         84 LeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIleGluIleGln 103
              :::|||||||||||||||||||:::|||||||:::::::|||||||||||||||||||||
Db        309 ATAGACCCCCGTGTGGTGCTTCTGGCCAACACAAAGAGTCAGTACAGCATTGAGATCCAA 368

Qy        104 AsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAspAsnHisPro 123
              ||||||||||:::||||||||||||||||||||||||||||||||||||||||||||||
Db        369 AATGTGGACATTTATGATGAGGGACCCTACACCTGCTCTGTGCAGACAGACAATCACCCC 428

Qy        124 LysThrSerArgValHisLeuIleValGlnValSerProLysIleValGluIleSerSer 143
              ||||||||||||||||||||||||||||||||||||   |||:::|||||||:::|||||||||
Db        429 AAAACCTCTCGTGTACATCTCATTGTGCAAGTTCCCCCTCGAATTGTTGATATTTCTTCA 488

Qy        144 AspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThrGlyArgPro 163
              :::|||:::::|||||||||:::|||:::||||||   ||||||||||||||||||||||
Db        489 AATATTGCTGTTAATGAAGGCAGTAATGTCAGCCTGATTTGCATTGCAACCGGGAGACCT 548

Qy        164 GluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheValSerGluAsp 183
              ||||||   |||   ||||||:::::||||||||||||   ||||||||||||||||||||
Db        549 GAACCCGTAGTGAACTGGAGATACTTGTCCCCTAAAGCACGGGGTTTTGTAAGTGAAGAT 608

Qy        184 GluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGluCysSerAla 203
              ||||||||||||||||   ||||||||||||||||||||||||   ||||||||||||||||
Db        609 GAGTACCTGGAAATCACAGGAATCACTAGGGAGCAGTCTGGAATATATGAATGCAGTGCG 668

Qy        204 SerAsnAspValAlaAlaProValValArgArgValLysValThrValAsnTyrProPro 223
              ||||||||||||:::||||||   ||||||||||||||:::||||||||||||||||||||
Db        669 TCCAATGATGTCTCGGCACCAGATGTCCGAAGGGTTAAATTAACAGTTAATTACCCACCA 728

Qy        224 TyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThrLeuGlnCys 243
              ||||||   :::|||:::      |||   |||:::|||  .  :::|||   ||||||||
Db        729 TACATTCTGGATGCACAGAACATCGGGGCTCCCCTTGGCCATCGAGGTATTTTGCAGTGT 788

Qy        244 GluAlaSerAlaValProSerAla-GluPheGlnTrpTyrLysAspAspLysArgLeuIl 263
              ||||||||||||||||||:::||| :::|||   ||||||||||:::||||||||||||
Db        789 GAAGCCTCTGCTGTACCTGCAGCCCGACTTCTTCTGGTACAAGGAAGACAAAAGGCTGAG 848

Qy        263 eGluGlyLysLys-GlyValLysValGlu 272
              :::     ::: ||||||||||||||||
Db        849 TGATTCATGGAGGGGGGGTCAAAGTAGAG 877

RESULT 7
AL533026
LOCUS       AL533026                1085 bp    mRNA    linear   EST 23-MAY-2003
DEFINITION  AL533026 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
            CS0DN005YD20 5-PRIME, mRNA sequence.
```

```
ACCESSION   AL533026
VERSION     AL533026.2  GI:31070858
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1085)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
COMMENT     On Feb 13, 2001 this sequence version replaced gi:12796519.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 6387.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DN005DB10QP1&cluster=6387.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DN005DB10QP1.
FEATURES             Location/Qualifiers
     source          1. .1085
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DN005YD20"
                     /tissue_type="ADULT BRAIN"
                     /dev_stage="adult"
                     /clone_lib="Homo sapiens ADULT BRAIN"
                     /note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-strand cDNA was digested with Not I and
                     cloned into the Not I and EcoRV sites of the pCMVSPORT 6
                     vector. Library was not normalized."
BASE COUNT      318 a    261 c    263 g    234 t      9 others
ORIGIN

Alignment Scores:
Pred. No.:              1.13e-110       Length:         1085
Score:                  1062.50         Matches:        211
Percent Similarity:     84.19%          Conservative:   2
Best Local Similarity:  83.40%          Mismatches:     0
Query Match:            58.83%          Indels:         40
DB:                     9               Gaps:           1

US-10-017-084A-523 (1-344) x AL533026 (1-1085)

Qy        132 ValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGlyAsn 151
              ::::::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 ATTAAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAAC 215

Qy        152 AsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArgHis 171
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 AATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACAC 275

Qy        172 IleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGlyIle 191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 ATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATC 335

Qy        192 ThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaProVal 211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 ACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTG 395

Qy        212 ValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGlyThr 231
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACA 455

Qy        232 GlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSerAla 251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        456 GGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCA 515

Qy        252 GluPheGlnTrpTyrLysAspAsp-Lys------------------------------ 260
              ||||||||||||||||||||||||| |||
Db        516 GAATTCCAGTGGTACAAGGATGACAAAAGAGCTGAAATCTCATTCACAGTTTGGTTATGA 575

Qy        260 ------------------------------------------------------------ 260

Db        576 TGGGAAAGCTTCCTCCCCATGGTGGACGAATGGTGTCAAAACGGCCAGTGGGATCAATCA 635

Qy        261 ------------------------ArgLeuIleGluGlyLysLysGlyValLysValGl 272
                                       ||||||||||||||||||||||||||||||||||
Db        636 GCCTGACTTGCTCGCAGAATCCTCCCGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGA 695

Qy        272 uAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyrGlyAs 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        696 AAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAA 755

Qy        292 nTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGl 312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        756 CTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGG 815

Qy        312 yProGlyAlaValSerGluValSerAsnGlyThrSerArgArgAlaGlyCysValTrpLe 332
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        816 TCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCT 875

Qy        332 uLeuProLeuLeuValLeuHisLeuLeuLeuLysPhe 344
              ||||||||||||||||||||||||||||||||||||
Db        876 GCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTT 912

RESULT 8
BU368328
LOCUS       BU368328                740 bp    mRNA    linear   EST 28-NOV-2002
DEFINITION  603789424F1 CSEQCHN72 Gallus gallus cDNA clone ChEST750p6 5', mRNA
            sequence.
ACCESSION   BU368328
VERSION     BU368328.1  GI:25876329
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 740)
  AUTHORS   Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
            Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
  TITLE     A Comprehensive Collection of Chicken cDNAs
  JOURNAL   Curr. Biol. 12 (22), 1965-1969 (2002)
  MEDLINE   22335534
   PUBMED   12445392
COMMENT     Contact: Simon Hubbard
            Department of Biomolecular Sciences
            University of Manchester Institute of Science and Technology (UMIST
            )
            PO Box 88, Manchester, M60 1QD, UK
            Tel: 01612008930
            Fax: 01612360409
            Email: Simon.Hubbard@umist.ac.uk.
FEATURES             Location/Qualifiers
     source          1. .740
                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /strain="Compton Line 15I"
                     /db_xref="taxon:9031"
                     /clone="ChEST750p6"
                     /sex="Female"
                     /tissue_type="cerebrum"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="CSEQCHN72"
                     /note="Organ: brain; Vector: pBluescript II KS(+); Site_1:
                     EcoRI; Site_2: NotI; This normalized library was
                     constructed from 1 million independent clones. cDNA
```

synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI , size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

BASE COUNT 170 a 234 c 207 g 129 t
ORIGIN

Alignment Scores:

Pred. No.:	3.8e-109	Length:	740
Score:	1047.00	Matches:	192
Percent Similarity:	91.85%	Conservative:	22
Best Local Similarity:	82.40%	Mismatches:	19
Query Match:	57.97%	Indels:	0
DB:	13	Gaps:	0

US-10-017-084A-523 (1-344) x BU368328 (1-740)

```
Qy        101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
              :::|||   :::||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CAGATCCACGACGTGGACGTGTACGATGAAGGGCCCTACACCTGCTCCGTGCAGACAGAC 62

Qy        121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db         63 AATCACCCCAAGACATCTCGCGTGCACCTCATTGTGCAAGTGTCGCCGAAAATTACCGAG 122

Qy        141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
              |||||||||||||||||||||||||||||   |||:::||||||||||||||||||||||
Db        123 ATCTCTTCTGACATCTCCATCAATGAAGGTGGCAACGTCAGCCTCACCTGCATAGCCACG 182

Qy        161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
              |||||||||:::||||||:::|||||||||||||||||||||||||||||||||||:::
Db        183 GGCAGGCCAGACCCCACAATCACCTGGAGACACATCTCGCCCAAAGCTGTGGGCTTCATC 242

Qy        181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
              |||||||||||||||||||||||  |||||||||||||||||||||||:::||||||
Db        243 AGCGAGGACGAGTACCTGGAGATCACAGGCATCACGAGGGAGCAGTCGGGCGAGTACGAG 302

Qy        201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
              ||||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db        303 TGCAGTGCCTCCAACGACGTGGCCGCGCCTGTCGTCCAGCGAGTCAAAGTCACCGTCAAC 362

Qy        221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
              ||||||||||||||||||:::||||||   |||||||||||||||||||||||||||||
Db        363 TACCCACCGTACATCTCGGATGCGAAGAGCACCGGTGTGCCGGTGGGGCAGAAGGGCATC 422

Qy        241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
              |||   ||||||||||||||||||||||||||:::||||||||||||||||||||||||
Db        423 CTGATGTGTGAAGCCTCCGCTGTGCCCTCCGCTGACTTCCAGTGGTACAAAGACGACAAG 482

Qy        261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
              ||||||   ||||||:::||||||:::|||||||||||:::   |||   |||:::|||
Db        483 CGGCTGGCTGAAGGACAGAAAGGGCTGAAGGTGGAAAACAAAGCCTTCTTCTCCCGACTG 542

Qy        281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||:::
Db        543 ACTTTCTTCAACGTCTCCGAGCAGGACTACGGCAACTACACCTGCGTGGCCTCCAACCAG 602

Qy        301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
              ||||||:::||||||||||||:::::::|||:::||||||||||||||||  :::   :::
Db        603 CTAGGAAACACCAACGCCAGCATGATCCTTTATGGCCCCGGTGCAGTGCACGATGGCAAC 662

Qy        321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeu 333
              :::|||      ||||||      |||   |||||||||
Db        663 AGCGGTGCGTGGCGGCGAGGCAGCTGTGCCTGGCTGCTG 701
```

RESULT 9

BU320256
LOCUS BU320256 840 bp mRNA linear EST 28-NOV-2002
DEFINITION 603851118F1 CSEQCHN62 Gallus gallus cDNA clone ChEST847d5 5', mRNA sequence.
ACCESSION BU320256
VERSION BU320256.1 GI:25828257
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 840)
AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E., Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE 22335534
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES Location/Qualifiers
source 1..840
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
/clone="ChEST847d5"
/dev_stage="36"
/lab_host="DH10B"
/clone_lib="CSEQCHN62"
/note="Organ: heads; Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI , size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

BASE COUNT 210 a 256 c 231 g 143 t
ORIGIN

Alignment Scores:

Pred. No.:	1.71e-108	Length:	840
Score:	1042.00	Matches:	194
Percent Similarity:	91.14%	Conservative:	22
Best Local Similarity:	81.86%	Mismatches:	20
Query Match:	57.70%	Indels:	1
DB:	13	Gaps:	0

US-10-017-084A-523 (1-344) x BU320256 (1-840)

```
Qy         98 TyrSerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerVal 117
              ||||||||||:::|||   :::||||||||||||||||||||||||||||||||||||
Db          2 TACAGCATCCAGATCCACGACGTGGACGTGTACGATGAAGGGCCCTACACCTGCTCCGTG 61

Qy        118 GlnThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLys 137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CAGACAGACAATCACCCCAAGACATCTCGCGTGCACCTCATTGTGCAAGTGTCGCCGAAA 121

Qy        138 IleValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCys 157
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Db        122 ATTACCGAGATCTCTTCTGACATCTCCATCAATGAAGGTGGCAACGTCAGCCTCACCTGC 181

Qy        158 IleAlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaVal 177

Db        182 ATAGCCACGGGCAGGCCAGACCCCACAATCACCTGGAGACACATCTCGCCCAAAGCTGTG 241

Qy        178 GlyPheValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGly 197

Db        242 GGCTTCATCAGCGAGGACGAGTACCTGGAGATCACAGGCATCACGAGGGAGCAGTCGGGC 301

Qy        198 AspTyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysVal 217

Db        302 GAGTACGAGTGCAGTGCCTCCAACGACGTGGCCGCGCCTGTCGTCCAGCGAGTCAAAGTC 361

Qy        218 ThrValAsnTyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGln 237

Db        362 ACCGTCAACTACCCACCGTACATCTCGGATGCGAAGAGCACCGGTGTGCCGGTGGGGCAG 421

Qy        238 LysGlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLys 257

Db        422 AAGGGCATCCTGATGTGTGAAGCCTCCGCTGTGCCCTCCGCTGACTTCCAGTGGTACAAA 481

Qy        258 AspAspLysArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeu 277

Db        482 GACGACAAGCGGCTGGCTGAAGGACAGAAAGGGCTGAAGGTGGAAAACAAAGCCTTCTTC 541

Qy        278 SerLysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAla 297

Db        542 TCCCGACTGACTTTCTTCAACGTCTCCGAGCAGGACTACGGCAACTACACCTGCGTGGCC 601

Qy        298 SerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSer 317

Db        602 TCCAACCAGCTAAAAAACACCAACGCCAGCATGATCCTTTATGGCCCCGGTGCAGTGCAC 661

Qy        318 GluValSerAsnGlyThrSer-ArgArgAlaGlyCysValTrpLeuLeu 333

Db        662 GATGGCAACAGCGGTGCCGTGGCGGCGAGGCAGCTGTGCCTGGCTGCTG 710

RESULT 10
BI755360
LOCUS       BI755360                 849 bp    mRNA    linear   EST 25-SEP-2001
DEFINITION  603024964F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5195750 5',
            mRNA sequence.
ACCESSION   BI755360
VERSION     BI755360.1  GI:15746938
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 849)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11489  row: o  column: 15
            High quality sequence stop: 848.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:5195750"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_114"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
                     male brains, age range 23-27 yo. Library is oligo-dT
                     primed and directionally cloned (EcoRV site is  destroyed
                     upon cloning). Average insert size 1.5 kb, insert size
                     range 1-3 kb.  Library is normalized and enriched for
                     full-length  clones and was constructed by C. Gruber
                     (Invitrogen).  Research  Genetics tracking code 019. Note:
                     this is a NIH_MGC Library."
BASE COUNT      218 a    239 c    227 g    165 t
ORIGIN

Alignment Scores:
Pred. No.:              2.63e-104       Length:             849
Score:                  1005.50         Matches:            190
Percent Similarity:     86.11%          Conservative:       27
Best Local Similarity:  75.40%          Mismatches:         33
Query Match:            55.68%          Indels:             2
DB:                     12              Gaps:               1

US-10-017-084A-523 (1-344) x BI755360 (1-849)

Qy          7 LysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeuAlaAlaLeuCysLeuPhe 26

Db         83 GAGATGTACCATCCTGCCTACTGGGTCGTCTTCTCGGCGACAACTGCCCTGCTCTTCATC 142

Qy         27 GlnGlyValProValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThr 46

Db        143 CCAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACG 202

Qy         47 ValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgVal 66

Db        203 GTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGTACCATAGATGACCGGGTAACCCGGGTG 262

Qy         67 AlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspPro 86

Db        263 GCCTGGCTAAACCGCAGCACCATCCTCTACGCTGGGAATGACAAGTGGTCCATAGACCCT 322

Qy         87 ArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAsp 106

Db        323 CGTGTGATCATCCTGGTCAATACACCAACCCAGTACAGCATCATGATCCAAAATGTGGAT 382

Qy        107 ValTyrAspGluGlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSer 126

Db        383 GTGTATGACGAAGGTCCGTACACCTGCTCTGTGCAGACAGACAATCATCCCAAAACGTCC 442

Qy        127 ArgValHisLeuIleValGlnValSerProLysIleValGluIleSerSerAspIleSer 146

Db        443 CGGGTTCACCTAATAGTGCAAGTTCCTCCTCAGATCATGAATATCTCCTCAGACATCACT 502

Qy        147 IleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThr 166

Db        503 GTGAATGAGGGAAGCAGTGTGACCCTGCTGTGTCTTGCTATTGGCAGACCAGAGCCAACT 562

Qy        167 ValThrTrpArgHisIleSer---ProLysAlaValGlyPheValSerGluAspGluTyr 185

Db        563 GTGACATGGAGACACCTGTCAGTCAACGAAGGCCAGGGCTTTGTAAGTGAGGATGAGTAC 622

Qy        186 LeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsn 205

Db        623 CTGGAGATCTCTGACATCAAGCGAGACCAGTCCGGGGAGTACGAATGCAGCGCCTTGAAC 682

Qy        206 AspValAlaAlaProValValArgArgVal-LysValThrValAsnTyrProProTyrIl 225

Db        683 GATGTCGCTGCGCCCGATGTGCGGAAAGTCACAAATCACTGTCAACTATCCTCCCTATAT 742

Qy        225 eSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAl 245

Db        743 CTCAAAAGCCAAGAACACTGGTGTTTCAGTCCGGCAGAAGGGCATCCTGAGCTGTGAAGC 802

Qy        245 aSerAlaValProSerAlaGluPheGlnTrpTyr 256
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Db        803 CTCTGCAGTCCCCATGGCTGAATTCCAGTGGTTC 836

RESULT 11
BI666583
LOCUS       BI666583                865 bp    mRNA    linear   EST 12-SEP-2001
DEFINITION  603291469F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5310833 5',
            mRNA sequence.
ACCESSION   BI666583
VERSION     BI666583.1  GI:15580816
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 865)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11787  row: j  column: 18
            High quality sequence stop: 742.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:5310833"
                     /tissue_type="hypothalamus"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_96"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
                     ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3',
                     size-selected for  average insert size 2.3 kb and
                     normalized to ROT 5. This is a primary library enriched
                     for full-length  clones and constructed using the
                     Cap-trapper method (Carninci, in preparation).  Library
                     constructed by M. Brownstein (NIMH/NHGRI, National
                     Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT      250 a    230 c    209 g    176 t
ORIGIN

Alignment Scores:
Pred. No.:              1.16e-101      Length:         865
Score:                  982.50         Matches:        207
Percent Similarity:     90.91%         Conservative:   3
Best Local Similarity:  89.61%         Mismatches:     13
Query Match:            54.40%         Indels:         8
DB:                     12             Gaps:           3

US-10-017-084A-523 (1-344) x BI666583 (1-865)

Qy          1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 242

Qy         21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 302

Qy         41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 362

Qy         61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 422

Qy         81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 482

Qy        101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 542

Qy        121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 602

Qy        141 IleSerSerAspIleSerIleAsnGluGlyAsn-AsnIleSerLeuThrCysIleAlaTh 160
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        603 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAAATATTAGCCTCACCTGCATAGCAAC 662

Qy        160 rGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVa 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        663 TGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGT 722

Qy        180 lSerGluAspGluTyrLeu---GluIleGlnGlyIleThrArgGlu-GlnSer---GlyA 198
              |||||||||||||||||||   |||          :::   |||:::|||||| ||||||   |||
Db        723 GAGTGAAGACGAACTACTTGGGAACTTCAGGGCCATCTCCCGGGAGCCAGTCAAGGGGAC 782

Qy        198 spTyrGluCys-SerAlaSerAsn-AspValAlaAla-ProValValArgArgValLysV 217
                     ||| |||||||||||| ||||||   ||| ||||||||||||||
Db        783 TAACGAGTTGCCAGTGCCTCCAATGGACGTTGGCGCGCCCCCGTGGTACGGAGAAGTACAC 842

Qy        217 alThrValAsnTyr---ProPro 223
                :::     |||   ||||||
Db        843 AGTCCACGGGATATTTTCCACCA 865

RESULT 12
CB582386
LOCUS       CB582386                601 bp    mRNA    linear   EST 03-APR-2003
DEFINITION  AMGNNUC:NRHY5-00414-H5-A W Rat hypothalamus (10471) Rattus
            norvegicus cDNA clone nrhy5-00414-h5 5', mRNA sequence.
ACCESSION   CB582386
VERSION     CB582386.1  GI:29526427
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 601)
  AUTHORS   Amgen EST Program.
  TITLE     Amgen Rat EST Program
  JOURNAL   Unpublished
COMMENT     Contact: Dan Fitzpatrick
            Amgen, Inc
            One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
            Tel: 805 447-4881
            Plate: 00414  row: h  column: 5.
FEATURES             Location/Qualifiers
     source          1. .601
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10116"
                     /clone="nrhy5-00414-h5"
                     /clone_lib="W Rat hypothalamus (10471)"
                     /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; W Rat
                     hypothalamus adult female Wistar rat avg. insert size 2.3
                     kb fraction 6 and 7"
BASE COUNT      151 a    157 c    162 g    130 t      1 others
ORIGIN

Alignment Scores:
Pred. No.:              8.25e-101      Length:         601
```

```
Score:                  973.00        Matches:       182
Percent Similarity:     98.95%        Conservative:    6
Best Local Similarity:  95.79%        Mismatches:      2
Query Match:            53.88%        Indels:          0
DB:                     14            Gaps:            0

US-10-017-084A-523 (1-344) x CB582386 (1-601)

Qy        155 LeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArgHisIleSerPro 174
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         15 CTCACTTGCATAGCCACAGGTAGACCGGAGCCTACAGTAACCTGGAGACATATTTCTCCC 74

Qy        175 LysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGlu 194
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         75 AAAGCTGTCGGCTTTGTGAGTGAGGATGAGTACCTGGAGATCCAGGGCATCACTCGGGAG 134

Qy        195 GlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgArg 214
              ||||||||||:::||||||||||||||||||||||||||||||||||||||||||||||
Db        135 CAGTCAGGCGAGTATGAGTGCAGCGCCTCCAACGACGTGGCAGCACCAGTCGTACGAAGA 194

Qy        215 ValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGlyThrGlyValPro 234
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        195 GTGAAGGTCACCGTGAACTATCCACCATACATCTCAGAAGCTAAGGGTACAGGTGTCCCC 254

Qy        235 ValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGln 254
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        255 GTGGGGCAGAAGGGGACTCTGCAGTGTGAAGCCTCGGCAGTCCCTTCAGCAGAATTTCAG 314

Qy        255 TrpTyrLysAspAspLysArgLeuIleGluGlyLysLysGlyValLysValGluAsnArg 274
              |||:::||||||||||||||||||:::||||||||||||||||||||||||||||||||
Db        315 TGGTTCAAGGATGACAAAAGACTGGTTGAAGGGAAGAAGGGAGTCAAAGTGGAAAACAGA 374

Qy        275 ProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThr 294
              ||||||||||||:::|||   ||||||||||||||||||||||||||||||||||||||
Db        375 CCTTTCCTTTCAAGACTCACCTTTTTCAACGTCTCTGAACACGACTATGGGAACTACACA 434

Qy        295 CysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGly 314
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        435 TGTGTGGCATCCAACAAGTTGGGCCACACCAATGCCAGCATCATGCTATTTGGCCCAGGT 494

Qy        315 AlaValSerGluValSerAsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuPro 334
              ||||||||||||||:::|||||||||||||||||||   |||:::|||||||||||||
Db        495 GCTGTCAGCGAGGTCAACAATGGGACGTCAAGGAGGGCANGCTGCATTTGGCTCCTCCCT 554

Qy        335 LeuLeuValLeuHisLeuLeuLeuLysPhe 344
              |||||||||||||||||||||||||||||||
Db        555 CTTCTGGTCTTACACCTGCTCCTCAAATTT 584


RESULT 13
BU365385
LOCUS       BU365385                793 bp    mRNA    linear   EST 28-NOV-2002
DEFINITION  603786031F1 CSEQCHN72 Gallus gallus cDNA clone ChEST742m7 5', mRNA
            sequence.
ACCESSION   BU365385
VERSION     BU365385.1  GI:25873373
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 793)
  AUTHORS   Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
            Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
  TITLE     A Comprehensive Collection of Chicken cDNAs
  JOURNAL   Curr. Biol. 12 (22), 1965-1969 (2002)
  MEDLINE   22335534
   PUBMED   12445392
COMMENT     Contact: Simon Hubbard
            Department of Biomolecular Sciences
            University of Manchester Institute of Science and Technology (UMIST
            )
            PO Box 88, Manchester, M60 1QD, UK
            Tel: 01612008930
            Fax: 01612360409
            Email: Simon.Hubbard@umist.ac.uk.
FEATURES             Location/Qualifiers
     source          1. .793
                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /strain="Compton Line 15I"
                     /db_xref="taxon:9031"
                     /clone="ChEST742m7"
                     /sex="Female"
                     /tissue_type="cerebrum"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="CSEQCHN72"
                     /note="Organ: brain; Vector: pBluescript II KS(+); Site_1:
                     EcoRI; Site_2: NotI; This normalized library was
                     constructed from 1 million independent clones. cDNA
                     synthesis was initiated using an oligo(dT) primer, using
                     methylated C in the first strand synthesis reaction.
                     Following this first strand reaction, double-stranded cDNA
                     was blunted, ligated to NotI adapters, digested with EcoRI
                     , size-selected, and cloned into the NotI and EcoRI
                     compatible sites of a custom modified MCS of the
                     pBluescript (KS+) vector. The library was normalized in 2
                     rounds using conditions adapted from Soares et al., PNAS
                     (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
                     (1996): 791, except that a significantly longer
                     reannealing hybridization was used."
BASE COUNT      194 a    230 c    231 g    138 t
ORIGIN

Alignment Scores:
Pred. No.:              1.36e-95      Length:        793
Score:                  929.00        Matches:       172
Percent Similarity:     91.43%        Conservative:   20
Best Local Similarity:  81.90%        Mismatches:     18
Query Match:            51.44%        Indels:          0
DB:                     13            Gaps:            0

US-10-017-084A-523 (1-344) x BU365385 (1-793)

Qy        124 LysThrSerArgValHisLeuIleValGlnValSerProLysIleValGluIleSerSer 143
              ||||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db          1 AAGACATCTCGCGTGCACCTCATTGTGCAAGTGTCGCCGAAAATTACCGAGATCTCTTCT 60

Qy        144 AspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThrGlyArgPro 163
              ||||||||||||||||||||||   |||:::|||||||||||||||||||||||||||||
Db         61 GACATCTCCATCAATGAAGGTGGCAACGTCAGCCTCACCTGCATAGCCACGGGCAGGCCA 120

Qy        164 GluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheValSerGluAsp 183
              :::|||||||:::|||||||||||||||||||||||||||||||||||:::|||||||||
Db        121 GACCCCACAATCACCTGGAGACACATCTCGCCCAAAGCTGTGGGCTTCATCAGCGAGGAC 180

Qy        184 GluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGluCysSerAla 203
              ||||||||||||||   ||||||||||||||||||||||:::|||||||||||||||||
Db        181 GAGTACCTGGAGATCACAGGCATCACGAGGGAGCAGTCGGGCGAGTACGAGTGCAGTGCC 240

Qy        204 SerAsnAspValAlaAlaProValValArgArgValLysValThrValAsnTyrProPro 223
              ||||||||||||||||||||||||||||:::|||||||||||||||||||||||||||||
Db        241 TCCAACGACGTGGCCGCGCCTGTCGTCCAGCGAGTCAAAGTCACCGTCAACTACCCACCG 300

Qy        224 TyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThrLeuGlnCys 243
              |||||||||:::||||||   ||||||||||||||||||||||||||   |||   |||
Db        301 TACATCTCGGATGCGAAGAGCACCGGTGTGCCGGTGGGGCAGAAGGGCATCCTGATGTGT 360

Qy        244 GluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLysArgLeuIle 263
              ||||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||
Db        361 GAAGCCTCCGCTGTGCCCTCCGCTGACTTCCAGTGGTACAAAGACGACAAGCGGCTGGCT 420

Qy        264 GluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeuIlePhePhe 283
              ||||||:::||||||:::|||||||||||||::   |||   |||:::|||   ||||||
Db        421 GAAGGACAGAAAGGGCTGAAGGTGGAAAACAAAGCCTTCTTCTCCCGACTGACTTTCTTC 480
```

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Qy        284 AsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLysLeuGlyHis 303
              ||||||||||||   ||||||||||||||||||||||||||||||:::|||||||:::
Db        481 AACGTCTCCGAGCAGGACTACGGCAACTACACCTGCGTGGCCTCCAACCAGCTAGGAAAC 540

Qy        304 ThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSerAsnGlyThr 323
              ||||||||||||:::::::|||::|||||||||||||||   :::   :::::|||
Db        541 ACCAACGCCAGCATGATCCTTTATGGCCCCGGTGCAGTGCACGATGGCAACAGCGGTGCG 600

Qy        324 SerArgArgAlaGlyCysValTrpLeuLeu 333
                  ||||||      |||   |||||||||
Db        601 TGGCGGCGAGGCAGCTGTGCCTGGCTGCTG 630

RESULT 14
BE263639
LOCUS       BE263639                545 bp    mRNA    linear   EST 13-JUL-2000
DEFINITION  601192064F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3536127 5',
            mRNA sequence.
ACCESSION   BE263639
VERSION     BE263639.1  GI:9137183
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 545)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Plate: LLCM217  row: p  column: 16
            High quality sequence stop: 545.
FEATURES             Location/Qualifiers
     source          1. .545
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3536127"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT      162 a    134 c    144 g    105 t
ORIGIN

Alignment Scores:
Pred. No.:                1.71e-95      Length:          545
Score:                    926.00        Matches:         180
Percent Similarity:       98.90%        Conservative:    0
Best Local Similarity:    98.90%        Mismatches:      1
Query Match:              51.27%        Indels:          1
DB:                       10            Gaps:            0

US-10-017-084A-523 (1-344) x BE263639 (1-545)

Qy         91 LeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyrAspGlu 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAG 60

Qy        111 GlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeu 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTC 120

Qy        131 IleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGly 150
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGG 180

Qy        151 AsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArg 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGA 240

Qy        171 HisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGly 190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGC 300

Qy        191 IleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaPro 210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATCACCAGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCC 360

Qy        211 ValValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGly 230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGT 420

Qy        231 ThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSer 250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCA 480

Qy        251 AlaGluPheGlnTrpTyrLysAspAspLysArgLeuIleGluGlyLys-LysGlyValLy 270
              ||||||||||||||||||||||||||||||||||||||||||||||| .||||||||||
Db        481 GCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAACGAAAGGGGTGAA 540

Qy        270 sVal 271
                ||||
Db        541 AGTG 544

RESULT 15
BG261691
LOCUS       BG261691                979 bp    mRNA    linear   EST 13-FEB-2001
DEFINITION  602373361F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4480983 5',
            mRNA sequence.
ACCESSION   BG261691
VERSION     BG261691.1  GI:12771416
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 979)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: The Cepko Laboratory
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10315  row: i  column: 16
            High quality sequence stop: 715.
FEATURES             Location/Qualifiers
     source          1. .979
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4480983"
                     /tissue_type="retina"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_94"
                     /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 3.3 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
BASE COUNT      231 a    261 c    289 g    198 t
```

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ORIGIN

Alignment Scores:
Pred. No.:                 4.69e-95      Length:         979
Score:                     925.50        Matches:        207
Percent Similarity:        87.70%        Conservative:   7
Best Local Similarity:     84.84%        Mismatches:     26
Query Match:               51.25%        Indels:         11
DB:                        10            Gaps:           2

US-10-017-084A-523 (1-344) x BG261691 (1-979)

Qy         12 IleSerTrpAlaIlePheThrGlyLeuAlaAlaLeuCysLeuPhe---------GlnGly 28
              :::   |||           ::::::       ||||||             |||
Db         67 CTGCCCTGGAAGTGCCTCGTGGTCGTGTCTCTCAGGCTGCTATTCCTTGTACCCACAGGA 126

Qy         29 ValProValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArg 48
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GTGCCGGTGCGTAGCGGAGATGCCACCTTTCCCAAAGCTATGGACAACGTGACGGTCAGG 186

Qy         49 GlnGlyGluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrp 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 CAGGGGGAGAGCGCCACCCTCAGGTGCACAATTGACAACCGAGTCACCCGGGTGGCCTGG 246

Qy         69 LeuAsnArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgVal 88
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 CTAAACCGCAGTACCATCCTCTATGCTGGAAATGACAAGTGGTGCCTAGATCCTCGTGTG 306

Qy         89 ValLeuLeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyr 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 GTCCTCCTGAGTAACACCCAGACCCAGTACAGCATTGAGATCCAGAATGTGGATGTGTAC 366

Qy        109 AspGluGlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgVal 128
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 GATGAGGGCCCTTATACCTGCTCGGTACAGACAGACAACCACCCTAAGACCTCCAGGTC- 425

Qy        129 HisLeuIleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsn 148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 CACCTCATTGTACAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAAT 485

Qy        149 GluGlyAsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThr 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 GAAGGGAACAACATCAGCCTCACTTGCATAGCCACAGGTAGACCGGAGCCTACAGTAACC 545

Qy        169 TrpArgHisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIle 188
              ||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db        546 TGGAGACATATTTCTCCCAAGGCCGTTGGCTTTGTGAGTGAGGATGAGTTCCTGGAGATC 605

Qy        189 GlnGlyIleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAla 208
              |||   |||||||||||||||||||||:::||||||||||||||     ||||||||||||
Db        606 CAGGACATCACTCGGGAACAGTCAGGCGAGTACGAGTGCAGCGCTC--AACGACGTGGCG 663

Qy        209 AlaProValValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAla 228
                 |||||||||||||||||||||     |||||||||    ||||||    |||:::
Db        664 G--ACCGTGGTACGAAGAGTGAAGGTCCC-GTGAACTATCA-CCATACAT-TCTCAGAAG 718

Qy        229 LysGlyThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaVal 248
                 |||  |||||||||   ||||||||||||   ||||||||||||         |||
Db        719 TTAGGGCCCGGTGTCCCGTGGGGGCAGAAGGGGCT-CTGCAGTGTGAGCTT---CGAGTC 774

Qy        249 ProSerAlaGlu 252
              ||||||   :::
Db        775 CCTTCGCCGGAT 786

Search completed: September 11, 2003, 05:12:23
Job time : 2518 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 11, 2003, 03:02:48 ; Search time 39 Seconds
(without alignments)
848.257 Million cell updates/sec

Title: US-10-017-084A-523
Perfect score: 1806
Sequence: 1 MKTIQPKMHNSISWAIFTGL.....RRAGCVWLLPLLVLHLLLKF 344

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1639.5	90.8	344	2	I56551	neurotrimin - rat
2	1285.5	71.2	338	2	JC1238	opioid-binding pro
3	1268	70.2	345	2	JC4025	opioid-binding cel
4	1266	70.1	345	2	S03199	opioid-binding pro
5	1259	69.7	345	2	JC1239	opioid-binding pro
6	936.5	51.9	338	2	JC5519	50K glycoprotein p
7	931.5	51.6	338	2	JC4776	limbic-system-asso
8	297.5	16.5	333	2	A31923	amalgam protein pr
9	283.5	15.7	725	1	IJMSNG	neural cell adhesi
10	283.5	15.7	1115	1	IJMSNL	neural cell adhesi
11	279.5	15.5	725	2	JE0099	neural cell adhesi
12	279.5	15.5	1091	1	IJCHNL	neural cell adhesi
13	278.5	15.4	4162	2	T42633	connectin/titin -
14	277.5	15.4	858	1	IJRTNC	neural cell adhesi
15	277.5	15.4	1088	1	IJXLNL	neural cell adhesi
16	276	15.3	761	1	IJHUNG	neural cell adhesi
17	275.5	15.3	853	1	IJBONC	neural cell adhesi
18	273.5	15.1	725	2	JE0100	neural cell adhesi
19	272.5	15.1	1323	2	PN0568	connectin 3B - chi
20	270.5	15.0	1092	1	JN0635	neural cell adhesi
21	261.5	14.5	1091	2	S01998	contactin precurso
22	259	14.3	7962	2	I38346	elastic titin - hu
23	254.5	14.1	5175	2	T20992	hypothetical prote
24	254.5	14.1	5198	2	T43290	hemicentin precurs
25	249.5	13.8	1040	2	A49356	transient axonal g
26	246.5	13.6	1018	2	A54744	contactin 1 precur
27	243.5	13.5	1021	2	A57112	contactin precurso
28	243.5	13.5	1036	2	S22383	axonin 1 precursor
29	241.5	13.4	1018	2	JC4211	neural adhesion pr
30	241.5	13.4	1020	2	S05944	neuronal cell surf
31	240	13.3	3707	2	S18252	heparan sulfate pr
32	235	13.0	662	2	T16525	hypothetical prote
33	234.5	13.0	1040	2	A34695	axonal glycoprotei
34	232.5	12.9	2783	2	T34416	hypothetical prote
35	230.5	12.8	868	2	A46512	CD22 homolog/B lym
36	227.5	12.6	1051	2	A39712	kinase-like protei
37	226	12.5	6642	2	T29757	protein UNC-89 - C
38	225	12.5	4391	2	A38096	perlecan precursor
39	221.5	12.3	862	2	I49583	differentiation an
40	221	12.2	1896	2	T08851	Down syndrome cell
41	220.5	12.2	898	2	A40114	fasciclin II precu
42	219	12.1	1091	2	A58532	glial cell membran
43	218.5	12.1	1612	2	T30805	duttl protein - mo
44	215.5	11.9	1239	1	A32579	neuroglian - fruit
45	214.5	11.9	1070	2	JC4593	protein-tyrosine k

ALIGNMENTS

RESULT 1
I56551
neurotrimin - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C;Accession: I56551
R;Struyk, A.F.; Canoll, P.D.; Wolfgang, M.J.; Rosen, C.L.; D'Eustachio, P.; Salzer, J
J. Neurosci. 15, 2141-2156, 1995
A;Title: Cloning of neurotrimin defines a new subfamily of differentially expressed n
A;Reference number: I56551; MUID:95198094; PMID:7891157
A;Accession: I56551
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-344 <RES>
A;Cross-references: EMBL:U16845; NID:g755184; PIDN:AAA67445.1; PID:g755185
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-ter

Query Match 90.8%; Score 1639.5; DB 2; Length 344;
Best Local Similarity 92.9%; Pred. No. 1.4e-113;
Matches 312; Conservative 9; Mismatches 12; Indels 3; Gaps 1;

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Qy         12 ISWAIFTGLAALCLF---QGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAW 68
              : |     ::   ||    ||||||||||||||||||||||||||||||||||||||||
Db          9 LPWKCLVVVSLRLLFLVPTGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAW 68

Qy         69 LNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRV 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 LNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRV 128

Qy        129 HLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEI 188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 HLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEI 188

Qy        189 QGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAV 248
              |||||||||:||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        189 QGITREQSGEYECSASNDVAAPVVRRVNVTVNYPPYISEAKGTGVPVGQKGTLQCEASAV 248

Qy        249 PSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASI 308
              |||||||:||||||:||||||||||||||:| ||||||||||||||||||||||||||||
Db        249 PSAEFQWFKDDKRLVEGKKGVKVENRPFLSRLTFFNVSEHDYGNYTCVASNKLGHTNASI 308

Qy        309 MLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
              ||||||||||:|||||||:|||||||||||||||||
Db        309 MLFGPGAVSEVNNGTSRRAGCIWLLPLLVLHLLLKF 344
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RESULT 2
JC1238
opioid-binding protein (clone DUZ1) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 19-May-2000
C;Accession: JC1238

```
R;Lippman, D.A.; Lee, N.M.; Loh, H.H.
Gene 117, 249-254, 1992
A;Title: Opioid-binding cell adhesion molecule (OBCAM)-related clones from a rat brain c
A;Reference number: JC1238; MUID:92347701; PMID:1339369
A;Accession: JC1238
A;Molecule type: mRNA
A;Residues: 1-338 <LIP>
A;Cross-references: GB:M88709; NID:g203245; PIDN:AAA40858.1; PID:g203246
A;Experimental source: brain
C;Genetics:
A;Gene: OBCAM
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin

  Query Match           71.2%;  Score 1285.5;  DB 2;  Length 338;
  Best Local Similarity  71.6%;  Pred. No. 1.8e-87;
  Matches  242;  Conservative   35;  Mismatches   60;  Indels    1;  Gaps    1;

Qy          8 MHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVA 67
              |:.   | :|:   ||    |||||||||||||||||||||||||||||||||:||||||
Db          1 MYHPAYWIVFSATTALLFIPGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDDRVTRVA 60

Qy         68 WLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSR 127
              |||||||||||||| :||||::| || ||||| |||||||||||||||||||||||||
Db         61 WLNRSTILYAGNDKWSIDPRVIILVNTPTQYSIMIQNVDVYDEGPYTCSVQTDNHPKTSR 120

Qy        128 VHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPK-AVGFVSEDEYL 186
              ||||||| |:|: |||||::|| ::::| |:| ||||||||||:| |   |||||||||
Db        121 VHLIVQVPPQIMNISSDITVNEISSVTLLCLAIGRPEPTVTWRHLSVKEGQGFVSEDEYL 180

Qy        187 EIQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEAS 246
              ||  | |:|||:||||| |||||| ||:||:|||||||||:|| ||| ||||| | ||||
Db        181 EISDIKRDQSGEYECSALNDVAAPDVRKVKITVNYPPYISKAKNTGVSVGQKGILSCEAS 240

Qy        247 AVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNA 306
              ||| |||||:|:| ||  |  ||::||:  :| | |||||| |||||||||:||||:|||
Db        241 AVPMAEFQWFKEDTRLATGLDGVRIENKGRISTLTFFNVSEKDYGNYTCVATNKLGNTNA 300

Qy        307 SIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
              || |:|||||  :  |  ||   |:||     |  :||
Db        301 SITLYGPGAVIDGVNSASRALACLWLSGTFFAHFFIKF 338


RESULT 3
JC4025
opioid-binding cell adhesion protein - human
C;Species: Homo sapiens (man)
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 17-Mar-2000
C;Accession: JC4025
R;Shark, K.B.; Lee, N.M.
Gene 155, 213-317, 1995
A;Title: Cloning, sequencing and localization to chromosome 11 of a cDNA encoding a huma
A;Reference number: JC4025; MUID:95237612; PMID:7721093
A;Accession: JC4025
A;Molecule type: mRNA
A;Residues: 1-345 <SHA>
A;Cross-references: GB:L34774; NID:g514373; PIDN:AAA36387.1; PID:g514374
A;Experimental source: brain
C;Comment: This protein binds opioid alkaloids in the presence of acidic lipids, exhibit
C;Genetics:
A;Gene: GDB:OPCML; OBCAM; OPCM
A;Cross-references: GDB:251677; OMIM:600632
A;Map position: 11pter-11qter
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin

  Query Match           70.2%;  Score 1268;  DB 2;  Length 345;
  Best Local Similarity  71.2%;  Pred. No. 3.7e-86;
  Matches  240;  Conservative   37;  Mismatches   56;  Indels    4;  Gaps    2;

Qy         12 ISWAIFTGLAALCLF---QGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAW 68
              : |     ::   ||    |||||||||||||||||||||||||||||||:|||||||
Db          9 LPWKCLVVVSLRLLFLVPTGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDDRVTRVAW 68

Qy         69 LNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRV 128
              ||||||||||||| :||||::| || ||||| |||||||||||||||||||||||||||
Db         69 LNRSTILYAGNDKWSIDPRVIILVNTPTQYSIMIQNVDVYDEGPYTCSVQTDNHPKTSRV 128

Qy        129 HLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPK-AVGFVSEDEYLE 187
              |||||| |:|: |||||::|||::::| |:| ||||||||||:| |   ||||||||||
Db        129 HLIVQVPPQIMNISSDITVNEGSSVTLLCLAIGRPEPTVTWRHLSVKEGQGFVSEDEYLE 188

Qy        188 IQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASA 247
              |  | |:|||:||||| |||||| ||:||:|||||||||:|| ||| ||||| | |||||
Db        189 ISDIKRDQSGEYECSALNDVAAPDVRKVKITVNYPPYISKAKNTGVSVGQKGILSCEASA 248

Qy        248 VPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNAS 307
              || |||||:|:: ||  |  |:::::|:  :| | |||||| |||||||||:||||:|||
Db        249 VPMAEFQWFKEETRLATGLDGMRIENKGRMSTLTFFNVSEKDYGNYTCVATNKLGNTNAS 308

Qy        308 IMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
              | |:|||||  :  |  ||   |:||    |: |  :||
Db        309 ITLYGPGAVIDGVNSASRALACLWLSGTLLAHFFIKF 345


RESULT 4
S03199
opioid-binding protein OPCAM precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 17-Mar-2000
C;Accession: S03199
R;Schofield, P.R.; McFarland, K.C.; Hayflick, J.S.; Wilcox, J.N.; Cho, T.M.; Roy, S.;
EMBO J. 8, 489-495, 1989
A;Title: Molecular characterization of a new immunoglobulin superfamily protein with
A;Reference number: S03199; MUID:89251576; PMID:2721489
A;Accession: S03199
A;Molecule type: mRNA
A;Residues: 1-345 <SCH>
A;Cross-references: EMBL:X12672; NID:g585; PIDN:CAA31192.1; PID:g586
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-ter
C;Keywords: transmembrane protein
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-345/Product: opioid-binding protein OPCAM #status predicted <MAT>

  Query Match           70.1%;  Score 1266;  DB 2;  Length 345;
  Best Local Similarity  71.6%;  Pred. No. 5.2e-86;
  Matches  240;  Conservative   34;  Mismatches   57;  Indels    4;  Gaps    2;

Qy         14 WAIFTGLAALCLF---QGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLN 70
              |     ::   ||    |||||||||||||||||||||||||||||||:|||||||||
Db         11 WKCLVVVSLRLLFLVPTGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDDRVTRVAWLN 70

Qy         71 RSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRVHL 130
              |||||||||||| :||||::| || ||||| |||||||||||||||||||||||||||||
Db         71 RSTILYAGNDKWSIDPRVIILVNTPTQYSIMIQNVDVYDEGPYTCSVQTDNHPKTSRVHL 130

Qy        131 IVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPK-AVGFVSEDEYLEIQ 189
              |||| |:|: |||||::|||::::| |:| ||||||||||:| |   ||||||||||
Db        131 IVQVPPQIMNISSDVTVNEGSSVTLLCLAIGRPEPTVTWRHLSVKEGQGFVSEDEYLEIS 190

Qy        190 GITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVP 249
              | |:|||:||||| |||||| ||:||:|||||||||:|| ||| ||||| | |||||||
Db        191 DIKRDQSGEYECSALNDVAAPDVRKVKITVNYPPYISKAKNTGVSVGQKGILSCEASAVP 250

Qy        250 SAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIM 309
              |||||:|:| ||  |  |:::||:  :| | |||||| |||||||||:|||| |||||
Db        251 MAEFQWFKEDTRLATGLDGMRIENKGHISTLTFFNVSEKDYGNYTCVATNKLGITNASIT 310

Qy        310 LFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
              |:|||| :  |  ||   |:||   |  |  :||
Db        311 LYGPGAVIDGVNSASRALACLWLSGTLFAHFFIKF 345


RESULT 5
JC1239
opioid-binding protein (clones SG8 and SG13) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 19-May-2000
```

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C;Accession: JC1239
R;Lippman, D.A.; Lee, N.M.; Loh, H.H.
Gene 117, 249-254, 1992
A;Title: Opioid-binding cell adhesion molecule (OBCAM)-related clones from a rat brain c
A;Reference number: JC1238; MUID:92347701; PMID:1339369
A;Accession: JC1239
A;Molecule type: mRNA
A;Residues: 1-345 <LIP>
A;Cross-references: GB:M88710; NID:g203247; PIDN:AAA40859.1; PID:g203248; GB:M88711; NID
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C;Keywords: transmembrane protein

  Query Match             69.7%;  Score 1259;  DB 2;  Length 345;
  Best Local Similarity   71.2%;  Pred. No. 1.7e-85;
  Matches  240;  Conservative   34;  Mismatches   59;  Indels    4;  Gaps    2;

Qy         12 ISWAIFTGLAALCLF---QGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAW 68
Db          9 LPWKCLVVVSLRLLFLVPTGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDDRVTRVAW 68

Qy         69 LNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRV 128
Db         69 LNRSTILYAGNDKWSIDPRVIILVNTPTQYSIMIQNVDVYDEGPYTCSVQTDNHPKTSRV 128

Qy        129 HLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPK-AVGFVSEDEYLE 187
Db        129 HLIVQVPPQIMNISSDITVNEISSVTLLCLAIGRPEPTVTWRHLSVKEGQGFVSEDEYLE 188

Qy        188 IQGITREQSGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASA 247
Db        189 ISDIKRDQSGEYECSALNDVAAPDVRKVKITVNYPPYISKAKNTGVSVGQKGILSCEASA 248

Qy        248 VPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNAS 307
Db        249 VPMAEFQWFKEDTRLATGLDGVRIENKGRISTLTFFNVSEKDYGNYTCVATNKLGNTNAS 308

Qy        308 IMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF 344
Db        309 ITLYGPGAVIDGVNSASRALACLWLSGTFFAHFFIKF 345

RESULT 6
JC5519
50K glycoprotein precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 17-Nov-2000
C;Accession: JC5519
R;Hancox, K.A.; Gooley, A.A.; Jeffrey, P.L.
Mol. Brain Res. 44, 273-285, 1997
A;Title: AvGp50, a predominantly axonally expressed glycoprotein, is a member of the IgL
A;Reference number: JC5519; MUID:97225899; PMID:9073169
A;Accession: JC5519
A;Molecule type: mRNA
A;Residues: 1-338 <HAN>
A;Experimental source: brain
C;Comment: This protein belongs to the IgLON's subfamily of cell adhesion molecules.
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C;Keywords: glycoprotein
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-338/Product: 50K glycoprotein #status predicted <MAT>
F;46-113/Domain: immunoglobulin homology <IMM1>
F;146-199/Domain: immunoglobulin homology <IMM2>
F;232-292/Domain: immunoglobulin homology <IMM3>
F;40,136,148,279,287,300,315/Binding site: carbohydrate (Asn) (covalent) #status predict

  Query Match             51.9%;  Score 936.5;  DB 2;  Length 338;
  Best Local Similarity   56.0%;  Pred. No. 1e-61;
  Matches  182;  Conservative   55;  Mismatches   83;  Indels    5;  Gaps    4;

Qy         20 LAALCLF-QGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTILYAG 78
Db         17 LRLLCLLPTGLPVRSVD--FTRGTDNITVRQGDTAILRCFVEDRSSKVAWLNRSGIIFAG 74

Qy         79 NDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKI 138
Db         75 EDKWSLDPRVELEKRSPLEYSLRIQKVDVYDEGSYTCSVQTQHHPKTSQVYLIVQVPPKI 134

Qy        139 VEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEIQGITREQSGD 198
Db        135 SNISSDITVNEGSNVTLVCMANGRPEPVITWRHLTPTGKEFEGEEEYLEILGITREQSGK 194

Qy        199 YECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWYKD 258
Db        195 YECKAANEVASADVKQVRVTVNYPPTITESKSNEAATGRQALLPCEASAVPTPDFEWYRD 254

Qy        259 DKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIMLFGPGAVSE 318
Db        255 DTR-INSANGLEIKSTGSQSLLMVANVTEEHYGNYTCVAANKLGVTNASLYLYRPG-TGR 312

Qy        319 VSNGTSRRAGCVWLLPLLVLHLLLK 343
Db        313 VDNGSVSLAVPLWLLAASLLCLLSK 337

RESULT 7
JC4776
limbic-system-associated membrane protein precursor - human
C;Species: Homo sapiens (man)
C;Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 19-May-2000
C;Accession: JC4776
R;Pimenta, A.F.; Fischer, I.; Levitt, P.
Gene 170, 189-195, 1996
A;Title: cDNA cloning and structural analysis of the human limbic-system-associated m
A;Reference number: JC4776; MUID:96235133; PMID:8666243
A;Accession: JC4776
A;Molecule type: mRNA
A;Residues: 1-338 <PIM>
A;Cross-references: GB:U41901; NID:g1276898; PIDN:AAC50569.1; PID:g1276899
A;Experimental source: brain
C;Comment: This is a neuronal surface glycoprotein distributed in cortical and subcon
C;Genetics:
A;Gene: lamp
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-ter
C;Keywords: brain; glycoprotein; membrane protein; phosphoprotein
F;1-7/Domain: signal sequence #status predicted <SIG>
F;333-338/Region: hydrophobic
F;40,66,136,148,279,287,300,315/Binding site: carbohydrate (Asn) (covalent) #status p
F;42,115,142,164,171,220,231/Binding site: phosphate (Thr) (covalent) #status predict
F;95,192,204,236,310/Binding site: phosphate (Ser) (covalent) #status predicted

  Query Match             51.6%;  Score 931.5;  DB 2;  Length 338;
  Best Local Similarity   55.4%;  Pred. No. 2.4e-61;
  Matches  180;  Conservative   60;  Mismatches   80;  Indels    5;  Gaps    4;

Qy         20 LAALCLF-QGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTILYAG 78
Db         17 LRLLCLLPTGLPVRSVD--FNRGTDNITVRQGDTAILRCVLEDKNSKVAWLNRSGIIFAG 74

Qy         79 NDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKI 138
Db         75 HDKWSLDPRVELEKRHSLEYSLRIQKVDVYDEGSYTCSVQTQHEPKTSQVYLIVQVPPKI 134

Qy        139 VEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEIQGITREQSGD 198
Db        135 SNISSDVTVNEGSNVTLVCMANGRPEPVITWRHLTPTGREFEGEEEYLEILGITREQSGK 194

Qy        199 YECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWYKD 258
Db        195 YECKAANEVSSADVKQVKVTVNYPPTITESKSNEATTGRQASLKCEASAVPAPDFEWYRD 254

Qy        259 DKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIMLFGPGAVSE 318
Db        255 DTR-INSANGLEIKSTEGQSSLTVTNVTEEHYGNYTCVAANKLGVTNASLVLFRPGSVRG 313

Qy        319 VSNGTSRRAGCVWLLPLLVLHLLLK 343
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Db        314 I-NGSISLAVPLWLLAASLLCLLSK 337

RESULT 8
A31923
amalgam protein precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 21-Jul-2000
C;Accession: A31923
R;Seeger, M.A.; Haffley, L.; Kaufman, T.C.
Cell 55, 589-600, 1988
A;Title: Characterization of amalgam: a member of the immunoglobulin superfamily from Dr
A;Reference number: A31923; MUID:89028670; PMID:3141062
A;Accession: A31923
A;Molecule type: DNA
A;Residues: 1-333 <SEE>
A;Cross-references: GB:M23561; NID:g156920; PIDN:AAA28367.1; PID:g156921
C;Genetics:
A;Gene: FlyBase:Ama
A;Cross-references: FlyBase:FBgn0000071

  Query Match             16.5%;  Score 297.5;  DB 2;  Length 333;
  Best Local Similarity   29.7%;  Pred. No. 1.4e-14;
  Matches   87;  Conservative   43;  Mismatches  136;  Indels   27;  Gaps   11;

Qy         44 NVTVRQGESATLRCTIDN-RVTRVAWLNR-------STILYAGNDKWCLDPR--VVLLSN 93
              :|    |:|    ||::       |:|  |        | :|   |      | |  | :
Db         33 DVVASVGDSVEFNCTVEEVGQLSVSWAKRPSESDTNSVVLSMRNILSLPDKRYNVTVTEG 92

Qy         94 TQTQ---YSIEIQNVDVYDEGPYTCSVQTDNHPK-TSRVHLIVQVSPKIVE-ISSDISIN 148
                  |:  |||::| | ||| | |          | | :: | ::  | | |        :
Db         93 PKTGSAIYTFRIQNIEVSDMGPYECQVLVSATEKVTKKLSLQIKTPPVIAENTPKSTLVT 152

Qy        149 EGNNISLTCIATGRPEPTVTWRH----ISPKAVGFVSEDEYLEIQGITREQSGDYECSAS 204
              || |: ||| | | |:|:|::|        : | | | :   :   | |: : |   | | | |
Db        153 EGQNLELTCHANGFPKPTISWAREHNAVMP-AGGHLLAEPTLRIRSVHRMDRGGYYCIAQ 211

Qy        205 NDVAAPVVRRVKVTVNYPPYIS-EAKGTGVPVGQKGTLQCEASAVPSAEFQWYKDDKRLI 263
              |     | | ::| | : | |: :       ·|    |:|      |:      |:|: |    |
Db        212 NGEGQPDKRLIRVEVEFRPQIAVQRPKIAQMVSHSAELECSVQGYPAPTVVWHKNGVPL- 270

Qy        264 EGKKGVKVENR-----PFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIMLF 311
              :  :  :| |            | |    :| | |:|:| | |:||||| :| : ||
Db        271 QSSRHHEVANTASSSGTTTSVLRIDSVGEEDFGDYYCNATNKLGHADARLHLF 323

RESULT 9
IJMSNG
neural cell adhesion molecule 1 precursor, GPI-anchored splice form - mouse
N;Alternate names: NCAM-120
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 31-Dec-2000
C;Accession: A29673; S00382; A44290
R;Barthels, D.; Santoni, M.J.; Wille, W.; Ruppert, C.; Chaix, J.C.; Hirsch, M.R.; Fontec
EMBO J. 6, 907-914, 1987
A;Title: Isolation and nucleotide sequence of mouse NCAM cDNA that codes for a Mr 79,00
A;Reference number: A29673; MUID:87246524; PMID:3595563
A;Accession: A29673
A;Molecule type: mRNA
A;Residues: 1-725 <BAR>
A;Cross-references: EMBL:Y00051; NID:g53342; PIDN:CAA68263.1; PID:g53343
R;Barbas, J.A.; Chaix, J.C.; Steinmetz, M.; Goridis, C.
EMBO J. 7, 625-632, 1988
A;Title: Differential splicing and alternative polyadenylation generates distinct NCAM t
A;Reference number: S00382; MUID:88283628; PMID:3396534
A;Accession: S00382
A;Molecule type: DNA
A;Residues: 642-656,'D',658-725 <BA2>
A;Cross-references: EMBL:X07195
R;Rougon, G.; Marshak, D.R.
J. Biol. Chem. 261, 3396-3401, 1986
A;Title: Structural and immunological characterization of the amino-terminal domain of m
A;Reference number: A44290; MUID:86140120; PMID:3512556
A;Accession: A44290
A;Molecule type: protein
A;Residues: 20-36 <ROU>
C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM
C;Comment: Several forms of NCAM are produced by alternative splicing. See also PIR:I
C;Genetics:
A;Gene: NCAM
A;Map position: 9
A;Introns: 701/1
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; i
C;Keywords: alternative splicing; cell adhesion; duplication; heparin binding; membra
F;1-19/Domain: signal sequence #status predicted <SIG>
F;34-98/Domain: immunoglobulin homology <IMM1>
F;132-191/Domain: immunoglobulin homology <IMM2>
F;152-156/Region: heparin binding #status predicted
F;161-165/Region: heparin binding #status predicted
F;228-290/Domain: immunoglobulin homology <IMM3>
F;263-272/Region: NCAM binding #status predicted
F;323-388/Domain: immunoglobulin homology <IMM4>
F;420-482/Domain: immunoglobulin homology <IMM5>
F;519-596/Domain: fibronectin type III repeat homology <FN3A>
F;625-685/Domain: fibronectin type III repeat homology <FN3B>
F;41-96,139-189,235-288,330-386,427-480/Disulfide bonds: #status predicted
F;222,316,348,424,450,479/Binding site: carbohydrate (Asn) (covalent) #status predict

  Query Match             15.7%;  Score 283.5;  DB 1;  Length 725;
  Best Local Similarity   25.8%;  Pred. No. 4.1e-13;
  Matches   75;  Conservative   45;  Mismatches  130;  Indels   41;  Gaps    7;

Qy         44 NVTVRQGESATLRCTIDNRVTRVAWLNRSTILYAGNDKWCLDPRVV--------LLSNTQ 95
              | |   |:| || |  |                 |:     |  |    :          |:
Db        222 NATANLGQSVTLVCDADG-------FPEPTM------SWTKDGEPIENEEEDERSRSSVS 268

Qy         96 TQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNNISL 155
                 : :|:||  ||  | |   :     : : :|| |    |||   :  :  ::     ::|
Db        269 DSSEVTIRNVDKNDEAEYVCIAENKAGEQDASIHLKVFAKPKITYVENQTAMELEEQVTL 328

Qy        156 TCIATGRPEPTVTWR---------------HISPKAVGFVSEDEYLEIQGITREQSGDYE 200
              || |:| | |::|||                 |: ::   ||    | : : |    :|:|
Db        329 TCEASGDPIPSITWRTSTRNISSEEQDLDGHMVVRSHARVSS---LTLKSIQYRDAGEYM 385

Qy        201 CSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWYKDDK 260
              |:|||  :        :  :  :         | :  :| ||  | |||   |::|  :
Db        386 CTASNTIGQD-SQSIDLEFQYAPKLQGPVAVYTWEGNQVNITCEVFAYPSATISWFRDGQ 444

Qy        261 RLIEGK-KGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIML 310
               |         :|: | :|  ·| |      ||:|:||| | | |::|   :   :|
Db        445 LLPSSNYSNIKIYNTPSASYLEVTPDSENDFGNYNCTAVNRIGQESLEFIL 495

RESULT 10
IJMSNL
neural cell adhesion molecule 1 precursor, long domain splice form - mouse
N;Alternate names: NCAM-180
N;Contains: neural cell adhesion molecule, short domain splice form (NCAM-140)
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 31-Dec-2000
C;Accession: A29673; S00844; S00384; A28281; A44290; S00383
R;Barthels, D.; Santoni, M.J.; Wille, W.; Ruppert, C.; Chaix, J.C.; Hirsch, M.R.; Fon
EMBO J. 6, 907-914, 1987
A;Title: Isolation and nucleotide sequence of mouse NCAM cDNA that codes for a Mr 79,
A;Reference number: A29673; MUID:87246524; PMID:3595563
A;Accession: A29673
A;Molecule type: mRNA
A;Residues: 1-548,'T',550-571,'T',573-574,'D',576-588,'MQPS',593,'S',595-599,'P',601,
A;Cross-references: EMBL:Y00051; NID:g53342; PIDN:CAA68263.1; PID:g53343
R;Santoni, M.J.; Barthels, D.; Barbas, J.A.; Hirsch, M.R.; Steinmetz, M.; Goridis, C.
Nucleic Acids Res. 15, 8621-8641, 1987
A;Title: Analysis of cDNA clones that code for the transmembrane forms of the mouse n
A;Reference number: S00844; MUID:88067687; PMID:3684567
A;Accession: S00844
A;Molecule type: mRNA
A;Residues: 529-809,1077-1115 <SAN>
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A;Cross-references: EMBL:X06328; NID:g53322; PIDN:CAA29641.1; PID:g817984
R;Barbas, J.A.; Chaix, J.C.; Steinmetz, M.; Goridis, C.
EMBO J. 7, 625-632, 1988
A;Title: Differential splicing and alternative polyadenylation generates distinct NCAM t
A;Reference number: S00382; MUID:88283628; PMID:3396534
A;Accession: S00384
A;Molecule type: DNA
A;Residues: 642-1115 <BAR>
A;Cross-references: EMBL:X07195
R;Barthels, D.; Vopper, G.; Wille, W.
Nucleic Acids Res. 16, 4217-4225, 1988
A;Title: NCAM-180, the large isoform of the neural cell adhesion molecule of the mouse,
A;Reference number: A28281; MUID:88247737; PMID:2454455
A;Accession: A28281
A;Molecule type: mRNA
A;Residues: 804-1081 <BA3>
A;Cross-references: EMBL:X07244; NID:g53321; PIDN:CAA30230.1; PID:g929720
R;Rougon, G.; Marshak, D.R.
J. Biol. Chem. 261, 3396-3401, 1986
A;Title: Structural and immunological characterization of the amino-terminal domain of m
A;Reference number: A44290; MUID:86140120; PMID:3512556
A;Accession: A44290
A;Molecule type: protein
A;Residues: 20-36 <ROU>
C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
C;Comment: Several forms of NCAM are produced by alternative splicing. See also PIR:IJMS
C;Genetics:
A;Gene: NCAM
A;Map position: 9
A;Introns: 643/3; 701/1; 770/2; 809/2; 1076/2
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C;Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; si
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1115/Product: neural cell adhesion molecule, long domain splice form #status experi
F;20-809,1077-1115/Product: neural cell adhesion molecule, short domain splice form #sta
F;20-711/Domain: extracellular #status predicted <EXT>
F;34-98/Domain: immunoglobulin homology <IMM1>
F;132-191/Domain: immunoglobulin homology <IMM2>
F;152-156/Region: heparin binding #status predicted
F;161-165/Region: heparin binding #status predicted
F;228-290/Domain: immunoglobulin homology <IMM3>
F;262-272/Region: NCAM binding #status predicted
F;323-388/Domain: immunoglobulin homology <IMM4>
F;420-482/Domain: immunoglobulin homology <IMM5>
F;519-596/Domain: fibronectin type III repeat homology <FN3A>
F;625-685/Domain: fibronectin type III repeat homology <FN3B>
F;712-729/Domain: transmembrane #status predicted <TMM>
F;730-1115/Domain: intracellular #status predicted <INT>
F;41-96,139-189,235-288,330-386,427-480/Disulfide bonds: #status predicted
F;222,316,348,424,450,479/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             15.7%;  Score 283.5;  DB 1;  Length 1115;
  Best Local Similarity   25.8%;  Pred. No. 7.1e-13;
  Matches   75;  Conservative   45;  Mismatches  130;  Indels   41;  Gaps    7;

Qy         44 NVTVRQGESATLRCTIDNRVTRVAWLNRSTILYAGNDKWCLDPRVV--------LLSNTQ 95
Db        222 NATANLGQSVTLVCDADG-------FPEPTM------SWTKDGEPIENEEEDERSRSSVS 268

Qy         96 TQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNNISL 155
Db        269 DSSEVTIRNVDKNDEAEYVCIAENKAGEQDASIHLKVFAKPKITYVENQTAMELEEQVTL 328

Qy        156 TCIATGRPEPTVTWR---------------HISPKAVGFVSEDEYLEIQGITREQSGDYE 200
Db        329 TCEASGDPIPSITWRTSTRNISSEEQDLDGHMVVRSHARVSS---LTLKSIQYRDAGEYM 385

Qy        201 CSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWYKDDK 260
Db        386 CTASNTIGQD-SQSIDLEFQYAPKLQGPVAVYTWEGNQVNITCEVFAYPSATISWFRDGQ 444

Qy        261 RLIEGK-KGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIML 310
Db        445 LLPSSNYSNIKIYNTPSASYLEVTPDSENDFGNYNCTAVNRIGQESLEFIL 495

RESULT 11
JE0099
neural cell adhesion molecule 1 - African clawed frog
N;Alternate names: N-CAM 1
C;Species: Xenopus laevis (African clawed frog)
C;Date: 19-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: JE0099
R;Kudo, M.; Takayama, E.; Tadakuma, T.; Shiokawa, K.
Biochem. Biophys. Res. Commun. 245, 127-132, 1998
A;Title: Molecular cloning of ssd-form neural cell adhesion molecules (N-CAMs) as the
A;Reference number: JE0099; MUID:98204770; PMID:9535795
A;Accession: JE0099
A;Molecule type: mRNA
A;Residues: 1-725 <KUD>
A;Cross-references: DDBJ:AB008162; NID:g3116226; PIDN:BAA25931.1; PID:g3116227
A;Experimental source: heart
C;Comment: This protein mediates and regulates various cell-cell interactions through
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; i
F;413-475/Domain: immunoglobulin homology <IMM>
F;512-589/Domain: fibronectin type III repeat homology <3FR>

  Query Match             15.5%;  Score 279.5;  DB 2;  Length 725;
  Best Local Similarity   27.9%;  Pred. No. 8.1e-13;
  Matches   80;  Conservative   50;  Mismatches  120;  Indels   37;  Gaps   11;

Qy         44 NVTVRQGESATLRCTIDN-RVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEI 102
Db        219 NATAKMAESVVLSCDADGFPDPEISWLKKGEPIEDGEEK---------ISFNEDQSEMTI 269

Qy        103 QNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGR 162
Db        270 HHVEKDDEAEYSCIANNQAGEAEATILLKVYAKPKITYVENKTAV-ELDEITLTCEASGD 328

Qy        163 PEPTVTW----RHISPKAV---GFVSEDEYLEIQGITRE-----QSGDYECSASNDVAAP 210
Db        329 PIPSITWRTAVRNISSEATTLDGHIVVKEHIRMSALTLKDIQYTDAGEYFCIASNPIGVD 388

Qy        211 VVRRVKVTVNYPPYISEAKGTGVPV------GQKGTLQCEASAVPSAEFQWYKDDKRLIE 264
Db        389 -MQAMYFEVQYAPKI---RG---PVVVYTWEGNPVNITCEVFAHPRAAVTWFRDGQLLPS 441

Qy        265 GK-KGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIML 310
Db        442 SNFSNIKIYSGPTSSSLEVNPDSENDFGNYNCTAINTIGHEFSEFIL 488

RESULT 12
IJCHNL
neural cell adhesion molecule long domain form precursor - chicken
N;Alternate names: NCAM-180
N;Contains: neural cell adhesion molecule, short domain form (NCAM-140)
C;Species: Gallus gallus (chicken)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 22-Jun-1999
C;Accession: A43613; B43613; A25435; B25435; A46550; S36950; A44369; A60852; S29668
R;Cunningham, B.A.; Hemperly, J.J.; Murray, B.A.; Prediger, E.A.; Brackenbury, R.; Ed
Science 236, 799-806, 1987
A;Title: Neural cell adhesion molecule: structure, immunoglobulin-like domains, cell
A;Reference number: A43613; MUID:87206190; PMID:3576199
A;Accession: A43613
A;Molecule type: mRNA
A;Residues: 1-175 <CU2>
A;Cross-references: GB:M15860
A;Accession: B43613
A;Molecule type: protein
A;Residues: 20-44;120-127;202-221;320-342;399-415;640-659;822-828 <CUN>
A;Note: Asn-222 probably binds carbohydrate; Asn-226 probably does not
R;Hemperly, J.J.; Murray, B.A.; Edelman, G.M.; Cunningham, B.A.
Proc. Natl. Acad. Sci. U.S.A. 83, 3037-3041, 1986
A;Title: Sequence of a cDNA clone encoding the polysialic acid-rich and cytoplasmic d
A;Reference number: A25435; MUID:86206089; PMID:3458261
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A;Accession: A25435
A;Molecule type: mRNA
A;Residues: 128-1091 <HEM>
A;Cross-references: GB:M13210
A;Accession: B25435
A;Molecule type: protein
A;Residues: 128-140;222-240;428-439;611-631;744-760;763-781;1080-1084 <HE2>
R;Murray, B.A.; Owens, G.C.; Prediger, E.A.; Crossin, K.L.; Cunningham, B.A.; Edelman, G
J. Cell Biol. 103, 1431-1439, 1986
A;Title: Cell surface modulation of the neural cell adhesion molecule resulting from alt
A;Reference number: A46550; MUID:87033934; PMID:3771645
A;Accession: A46550
A;Molecule type: DNA
A;Residues: 810-1070 <MUR>
A;Cross-references: GB:X04479
R;Sasner, M.; Covault, J.
submitted to the EMBL Data Library, February 1993
A;Reference number: S36950
A;Accession: S36950
A;Molecule type: DNA
A;Residues: 1-17 <SAS>
A;Cross-references: EMBL:X70342; NID:g417631; PIDN:CAA49807.1; PID:g417632
R;Colwell, G.; Li, B.; Forrest, D.; Brackenbury, R.
Genomics 14, 875-882, 1992
A;Title: Conserved regulatory elements in the promoter region of the N-CAM gene.
A;Reference number: A44369; MUID:93122797; PMID:1478668
A;Accession: A44369
A;Molecule type: DNA
A;Residues: 1-17 <COF>
A;Cross-references: EMBL:Z12128; NID:g63653; PIDN:CAA78113.1; PID:g63654
A;Experimental source: White Leghorn
R;Cole, G.J.; Loewy, A.; Cross, N.V.; Akeson, R.; Glaser, L.
J. Cell Biol. 103, 1739-1744, 1986
A;Title: Topographic localization of the heparin-binding domain of the neural cell adhes
A;Reference number: A60852; MUID:87057627; PMID:2430978
A;Accession: A60852
A;Molecule type: protein
A;Residues: 20-29 <COL>
R;Rao, Y.; Wu, X.F.; Gariepy, J.; Rutishauser, U.; Siu, C.H.
J. Cell Biol. 118, 937-949, 1992
A;Title: Identification of a peptide sequence involved in homophilic binding in the neur
A;Reference number: A43280; MUID:92363934; PMID:1380002
A;Contents: annotation; homophilic binding region
C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
C;Comment: Various forms of NCAM are produced by alternative splicing.
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C;Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; si
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1091/Product: neural cell adhesion molecule, long domain form #status experimental
F;20-809,1071-1091/Product: neural cell adhesion molecule, short domain form #status exp
F;20-711/Domain: extracellular #status predicted <EXT>
F;34-98/Domain: immunoglobulin homology <IMM1>
F;132-191/Domain: immunoglobulin homology <IMM2>
F;152-156/Region: heparin binding #status predicted
F;151-165/Region: heparin binding #status predicted
F;228-289/Domain: immunoglobulin homology <IMM3>
F;262-271/Region: NCAM binding #status experimental
F;322-387/Domain: immunoglobulin homology <IMM4>
F;419-481/Domain: immunoglobulin homology <IMM5>
F;518-595/Domain: fibronectin type III repeat homology <FN3A>
F;624-685/Domain: fibronectin type III repeat homology <FN3B>
F;712-729/Domain: transmembrane #status predicted <TMM>
F;730-1091/Domain: intracellular #status predicted <INT>
F;41-96,139-189,235-287,329-385,426-479/Disulfide bonds: #status predicted
F;222/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;315,347,423,449,478/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match           15.5%;  Score 279.5;  DB 1;  Length 1091;
  Best Local Similarity   26.0%;  Pred. No. 1.4e-12;
  Matches   78;  Conservative   52;  Mismatches  131;  Indels   39;  Gaps    9;

Qy         31 VRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTILYAGNDKWCLDPRVVL 90
              ||:  :|     | |    :| || |  |           |:       | |   :
```

```
Db        214 VRARQSTM-----NATANLSQSVTLACDADG-------FPEPTM------TWTKDGEPIE 255

Qy         91 LSNTQTQYSIE-------IQNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKIVEISS 143
                : : :||         |: ||  ||  | |  :     : : :|| |   |||  : :
Db        256 QEDNEEKYSFNYDGSELIIKKVDKSDEAEYICIAENKAGEQDATIHLKVFAKPKITYVEN 315

Qy        144 DISINEGNNISLTCIATGRPEPTVTW----RHISPKAV---GFVSEDEYLEIQGITREQ- 195
              ::   : |:||| |:| | |:::||    |:|| :     | :    :  :  :| ::
Db        316 KTAMELEDQITLTCEASGDPIPSITWKTSTRNISNEEKTLDGRIVVRSHARVSSLTLKEI 375

Qy        196 ----SGDYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSA 251
                  :|:| |:||| :     : : :.| | | :          | :  : ||  | |||
Db        376 QYTDAGEYVCTASNTIGQD-SQAMYLEVQYAPKLQGPVAVYTWEGNQVNITCEVFAYPSA 434

Qy        252 EFQWYKDDKRLIEGK-KGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIML 310
                |::| : |      :|: | |  | |     ||:|:||| | | |::|  ::  :|
Db        435 VISWFRDGQLLPSSNYSNIKIYNTPSASYLEVTPDSENDFGNYNCTAVNRIGQESSEFIL 494


RESULT 13
T42633
connectin/titin - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C;Accession: T42633
R;Yajima, H.; Ohtsuka, H.; Kawamura, Y.; Kume, H.; Murayama, T.; Abe, H.; Kimura, S.;
Biochem. Biophys. Res. Commun. 223, 160-164, 1996
A;Title: A 11.5-kb 5'-terminal cDNA sequence of chicken breast muscle connectin/titin
A;Reference number: Z22221; MUID:96254045; PMID:8660363
A;Accession: T42633
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-4162 <YAJ>
A;Cross-references: EMBL:D83390; NID:g1513029; PIDN:BAA11908.1; PID:g1513030
A;Experimental source: breast muscle
C;Keywords: skeletal muscle

  Query Match           15.4%;  Score 278.5;  DB 2;  Length 4162;
  Best Local Similarity   27.3%;  Pred. No. 8.9e-12;
  Matches   78;  Conservative   38;  Mismatches  145;  Indels   25;  Gaps    7;

Qy         37 TFPKAMDNVTVRQGESATLRCTI-DNRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQ 95
              :| |  :  :|  ||: |    :  :    | |   |  | |  |:           |
Db       3747 SFVKKPEPFNVLSGENITFTSIVKGSPPLEVKWFRGSIELAPGHK-----------CNIT 3795

Qy         96 TQYSI---EIQNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNN 152
                | :   |: :|     | ||| |  :    :   || |:   | |   :|:|: :| |
Db       3796 LQDSVAELELFDVQPLQSGDYTCQVSNEAGKISCTTHLFVKEPAKFVMKVNDLSVEKGKN 3855

Qy        153 ISLTCIATGRPEPTVTW-------RHISPKAVGFVSEDEYLEIQGITREQSGDYECSASN 205
              : | |  || ||  :|||       :|    ::        |||      |  | | |   |
Db       3856 LILECTYTGTPPISVTWKKNGVILKHSEKCSITTTETSAILEIPNSKLEDQGQYSCHIEN 3915

Qy        206 DVAAPVVRRVKVTVNYPPY-ISEAKGTGVPVGQKGTLQCEASAVPSAEFQWYKDDKRLIE 264
              |      | :|:  ||| ::  :   | ||   :|||: :  |     ||| | :|
Db       3916 DSGQDNCHGA-ITILEPPYFVTPLEPVQVTVGDSASLQCQVAGTPEMIVSWYKGDTKL-R 3973

Qy        265 GKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIML 310
              |  ||:  :  :: |:|  |  | | | |  | :|  :| :|
Db       3974 GTATVKMHFKNQVATLVFSQVDSDDSGEYICKVENTVGEATSSSLL 4019


RESULT 14
IJRTNC
neural cell adhesion molecule short domain form precursor - rat
N;Alternate names: NCAM-140
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 22-Jun-1999
C;Accession: S00846; B37795; I58136
R;Small, S.J.; Shull, G.E.; Santoni, M.J.; Akeson, R.
J. Cell Biol. 105, 2335-2345, 1987
A;Title: Identification of a cDNA clone that contains the complete coding sequence fo
A;Reference number: S00846; MUID:88059265; PMID:3680385
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A;Accession: S00846
A;Molecule type: mRNA
A;Residues: 1-858 <SMA>
A;Cross-references: EMBL:X06564
R;Small, S.J.; Akeson, R.
J. Cell Biol. 111, 2089-2096, 1990
A;Title: Expression of the unique NCAM VASE exon is independently regulated in distinct
A;Reference number: A37795; MUID:91035620; PMID:1699951
A;Accession: B37795
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 340-381 <SM2>
R;Small, S.J.; Haines, S.L.; Akeson, R.A.
Neuron 1, 1007-1017, 1988
A;Title: Polypeptide variation in an N-CAM extracellular immunoglobulin-like fold is dev
A;Reference number: I58136; MUID:90166485; PMID:2483093
A;Accession: I58136
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 355-364 <RES>
A;Cross-references: GB:M32611; NID:g205643; PIDN:AAA41679.1; PID:g205644
C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
C;Comment: Various forms of NCAM are produced by alternative splicing.
C;Genetics:
A;Gene: NCAM
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C;Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; si
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F;20-858/Product: neural cell adhesion molecule, short domain form #status predicted <MA
F;20-721/Domain: extracellular #status predicted <EXT>
F;34-98/Domain: immunoglobulin homology <IMM1>
F;132-191/Domain: immunoglobulin homology <IMM2>
F;152-156/Region: heparin binding #status predicted
F;161-165/Region: heparin binding #status predicted
F;228-290/Domain: immunoglobulin homology <IMM3>
F;263-272/Region: NCAM binding #status predicted
F;323-398/Domain: immunoglobulin homology <IMM4>
F;430-492/Domain: immunoglobulin homology <IMM5>
F;529-606/Domain: fibronectin type III repeat homology <FN3A>
F;635-695/Domain: fibronectin type III repeat homology <FN3B>
F;722-739/Domain: transmembrane #status predicted <TMM>
F;740-858/Domain: intracellular #status predicted <INT>
F;41-96,139-189,235-288,330-396,437-490/Disulfide bonds: #status predicted
F;222,316,348,434,460,489/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             15.4%;  Score 277.5;  DB 1;  Length 858;
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Qy         44 NVTVRQGESATLRCTIDN-RVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEI 102
              | |   |:| || |  |           ::|        :   |    : |: :: : :|
Db        222 NATANLGQSVTLVCDADGFPEPTMSWTKDGEPIENEEE----DDEKHIFSDDSSE--LTI 275

Qy        103 QNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGR 162
              :||| ||  | |  :      : : :|| |   ||| : :  ::    ::||| |:|
Db        276 RNVDKNDEAEYVCIAENKAGEQDASIHLKVFAKPKITYVENQTAMELEEQVTLTCEASGD 335

Qy        163 PEPTVTWR-----------------------HISPKAVGFVSEDEYLEIQGITREQSG 197
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Qy        198 DYECSASNDVAAPVVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWYK 257
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Qy        258 DDKRLIEGK-KGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIML 310
              | : |      :|: | | | |        ||:|:||| | | |::|  :  :|
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RESULT 15
IJXLNL
neural cell adhesion molecule long domain form precursor - African clawed frog
N;Alternate names: NCAM-180
N;Contains: neural cell adhesion molecule, short domain form (NCAM-140)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 22-Jun-1999
C;Accession: S09600
R;Krieg, P.A.; Sakaguchi, D.S.; Kintner, C.R.
Nucleic Acids Res. 17, 10321-10335, 1989
A;Title: Primary structure and developmental expression of a large cytoplasmic domain
A;Reference number: S09600; MUID:90098871; PMID:2481269
A;Accession: S09600
A;Molecule type: mRNA
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A;Cross-references: EMBL:M25696; NID:g214609; PIDN:AAA49909.1; PID:g214610
A;Note: the authors translated the codon AAA for residue 970 as Leu
C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM
C;Comment: Several forms of NCAM are produced by alternative splicing.
C;Genetics:
A;Gene: NCAM
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; i
C;Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding;
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1088/Product: neural cell adhesion molecule, long domain form #status predicted
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F;20-705/Domain: extracellular #status predicted <EXT>
F;34-95/Domain: immunoglobulin homology <IMM1>
F;129-188/Domain: immunoglobulin homology <IMM2>
F;149-153/Region: heparin binding #status predicted
F;158-162/Region: heparin binding #status predicted
F;225-284/Domain: immunoglobulin homology <IMM3>
F;317-381/Domain: immunoglobulin homology <IMM4>
F;413-475/Domain: immunoglobulin homology <IMM5>
F;512-589/Domain: fibronectin type III repeat homology <FN3A>
F;618-679/Domain: fibronectin type III repeat homology <FN3B>
F;706-723/Domain: transmembrane #status predicted <TMM>
F;724-1088/Domain: intracellular #status predicted <INT>
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Qy         44 NVTVRQGESATLRCTIDN-RVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEI 102
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Qy        103 QNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGR 162
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Qy        163 PEPTVTW----RHISPKAV---GFVSEDEYLEIQGITRE-----QSGDYECSASNDVAAP 210
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Qy        211 VVRRVKVTVNYPPYISEAKGTGVPV------GQKGTLQCEASAVPSAEFQWYKDDKRLIE 264
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Qy        265 GK-KGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIML 310
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Search completed: September 11, 2003, 03:05:44
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